

OM protein - protein search, using sw model
Run on: August 28, 2006, 17:25:54 ; Search time 196 Seconds
(without alignments)
620.508 Million cell updates/sec

Title: US-10-006-867-2

Perfect score: 1392
Sequence: 1 MMWFQQGLSFLPSALVWTS.....YDTAPCPINNERTLLSRDI 266
Scoring table: BLOSUM62

Searched: Gapop 10.0 , Gapext 0.5
2589679 seqs, 457216429 residues
Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database : A_Geneseq_8.*

1: Geneseqp1980s.*

2: Geneseqp1990s.*

3: Geneseqp2000s.*

4: Geneseqp2001s.*

5: Geneseqp2002s.*

6: Geneseqp2003as.*

7: Geneseqp2003bs.*

8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

No. Score Match Length DB ID Description

RESULT 1

ID AAY66636 standard; protein; 266 AA.

DE Membrane-bound protein PRO180.

PN W09563088-A2.

PD 09-DEC-1999.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1392; DB 3; Length 266;

Best Local Similarity 100.0%; Pred. No. 5e-149;

RESULT 2

ID AAU29028 standard; protein; 266 AA.

DE Human PRO polypeptide sequence #5.

PN W0200168848-A2.

PD 20-SEP-2001.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1392; DB 4; Length 266;

Best Local Similarity 100.0%; Pred. No. 5e-149;

RESULT 3

ID AAM39568 standard; protein; 266 AA.

DE Human polypeptide SEQ ID NO 2713.

PN W0200153312-A1.

PD 26-JUL-2001.

PA (HYSE-) HYSEQ INC.

Query Match 100.0%; Score 1392; DB 4; Length 266;

Best Local Similarity 100.0%; Pred. No. 5e-149;

RESULT 4

ID AAB65159 standard; protein; 266 AA.

DE Human PRO180 (UNQ154) protein sequence SEQ ID NO:23.

PN W0200073454-A1.

PD 07-DEC-2000.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1392; DB 4; Length 266;

Best Local Similarity 100.0%; Pred. No. 5e-149;

RESULT 5

ID ABB90338 standard; protein; 266 AA.

DE Human polypeptide SEQ ID NO 2714.

PN W0200190304-A2.

PD 29-NOV-2001.

PA (HUMA-) HUMAN GENOME SCI INC.

Query Match 100.0%; Score 1392; DB 5; Length 266;

Best Local Similarity 100.0%; Pred. No. 5e-149;

RESULT 6

ID ABG95851 standard; protein; 266 AA.

DE Human secreted/transmembrane protein PRO180.

PD 13-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 17
ID ABU9831 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003036147-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 18
ID ABR68080 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003027264-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 19
ID ADA57044 standard; protein; 266 AA.
DE Human secreted protein #327.
PN WO2002102994-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 20
ID ABU60483 standard; protein; 266 AA.
DE Human secreted/transmembrane protein, #9.
PN US2002160384-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 21
ID ABU96133 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003036144-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 22
ID ABU92564 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003036149-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 23
ID ABO08641 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003044923-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 24
ID ABO02693 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003040062-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 25
ID ABR74847 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003040056-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 26
ID ABR94609 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003044926-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 27
ID ABU13865 standard; protein; 266 AA.
DE Human PRO180 polypeptide.
PN US2002103125-A1.
PD 01-AUG-2002.
PA (GETH) GENENTECH LTD.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 28
ID ABU85582 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003036140-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 29
ID ABU98742 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003013153-A1.
PD 16-JAN-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 30
ID ABU97957 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003017544-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 31
ID ABU91663 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003027277-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 32
ID ABU89356 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003036141-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 33
ID ABU86197 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003036146-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 34
ID ABU67410 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003036162-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 35
ID ABU80438 standard; protein; 266 AA.
DE Human PRO protein #5.
PN US2003036137-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 36
ID ABU72450 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.

PN US2003003531-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 37
ID ABUS90876 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003018173-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 38
ID ABO33935 standard; protein; 266 AA.
DE Human secreted/transmembrane protein PRO180.
PN US2003009013-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 39
ID ABR99356 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003040063-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 40
ID ABR98746 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003040064-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 41
ID ABO16269 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003027267-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 42
ID ABR92169 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003031610-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 43
ID ABO18810 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003044925-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 44
ID ABR78231 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003054474-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 45
ID ABU71952 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003018183-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 46
ID ABO19115 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.

ID ABUS4967 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003032114-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 47
ID ABO00106 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003032101-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 48
ID ABO11438 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003036124-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 49
ID ABO02083 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003040054-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 50
ID ADA4098 standard; protein; 266 AA.
DE Human secreted protein.
PN WO2002102993-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 51
ID ABUS8657 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003036133-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 52
ID ABUS3352 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003036134-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 53
ID ABO06153 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003022294-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 54
ID ABR59189 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003027275-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 55
ID ABO09251 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003027324-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 56
ID ABO19115 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.

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PN US2003036118-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 57
ID ABO11133 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003036123-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 58
ID ABR66751 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003036148-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 59
ID ABO15964 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003040060-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 60
ID ABO13670 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003044916-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 61
ID ABU71506 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180.
PN US2003013855-A1.
PD 16-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 62
ID ABU65573 standard; protein; 266 AA.
DE Human secreted/transmembrane protein, SEQ ID 10.
PN US2003036156-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 63
ID ABO07421 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003032117-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 64
ID ABO03608 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003036128-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 65
ID ABR67056 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003027266-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 66
ID ABO13980 standard; protein; 266 AA.
DE Novel human secreted protein #9.
PN US2003028003-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 67
ID ABO15659 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003054483-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 68
ID ABUS5940 standard; protein; 266 AA.
DE Human secreted/transmembrane protein, PRO180.
PN US2003022298-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 69
ID ABU72287 standard; protein; 266 AA.
DE Human PRO polypeptide #1.
PN US2002182638-A1.
PD 05-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 70
ID ABU65268 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003032102-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 71
ID ABU95213 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003036117-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 72
ID ABU71116 standard; protein; 266 AA.
DE Human PRO180 protein.
PN US2003036143-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 73
ID ABO07726 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003032130-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 74
ID ABR69967 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003028003-A1.
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PN US2003032138-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 75
ID ABR69300 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003036132-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 76
ID ABO01441 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003008353-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 77
ID ABU81243 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003017542-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 78
ID ABR60040 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003032137-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 79
ID ABU90960 standard; protein; 266 AA.
DE Human PRO polypeptide #1.
PN US2003018168-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 80
ID ABR67775 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003027269-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 81
ID ABR65163 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003027268-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 82
ID ABR68385 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003027274-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 83
ID ABR71797 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003032135-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 84
ID ABU59199 standard; protein; 266 AA.

DE Human secreted/transmembrane protein, #9.
PN US2003027162-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 85
ID ABU85277 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003022295-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 86
ID ABU88967 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003022297-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 87
ID ABU83047 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003032105-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 88
ID ABU94903 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003032123-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 89
ID ABU90451 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003032108-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 90
ID ABU3962 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003032111-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 91
ID ABU93613 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003032119-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 92
ID ABO25896 standard; protein; 266 AA.
DE Human PRO180 polypeptide.
PN US2002127576-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 93
ID ABR64858 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003027263-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 94
ID ABO27281 standard; protein; 266 AA.
DE Human secreted/transmembrane polypeptide PRO180.

PN US2003009012-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 95
ID ABR68690 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US200302721-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 96
ID ABO06506 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003036125-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 97
ID ABR99051 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003040068-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 98
ID ABU56935 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003027280-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 99
ID ABU85887 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003022300-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 100
ID ABU82174 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003036136-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 101
ID ABU87185 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003036138-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 102
ID ABU83657 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003032109-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 103
ID ABO08031 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003040066-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 104
ID ABU92476 standard; protein; 266 AA.
DE Human secreted/transmembrane protein PRO180.
PN US2003045684-A1.
PD 06-MAR-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 105
ID ABU81742 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003032104-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 106
ID ABU65906 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003036157-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 107
ID ABU81146 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180.
PN US2003027212-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 108
ID ABR59735 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003032120-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 109
ID ABU93923 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003036155-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 110
ID ABU99776 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003022296-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 111
ID ABR66446 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003027281-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 112
ID ABR90864 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003040058-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 113
ID ABO53261 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003027986-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 114
ID ABU58905 standard; protein; 266 AA.
DE Human secreted/transmembrane protein, #9.
PN US2002142961-A1.

PD 03-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 115
ID ABU94291 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003017540-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 116
ID ABU79173 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003032106-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 117
ID ABU86502 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003032129-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 118
ID ABU86807 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003032131-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 119
ID ABU94596 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003032103-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 120
ID ABO04523 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003032107-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 121
ID ABR70272 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003032139-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 122
ID ABU92283 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003022187-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 123
ID ABU98437 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003022301-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 124
ID ABR65836 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003036165-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 125
ID ABR64553 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003027262-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 126
ID ABU59348 standard; protein; 266 AA.
DE Novel human secreted or transmembrane protein PRO180.
PN US2003027985-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 127
ID ABU79478 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003032110-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 128
ID ABU92869 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003036142-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 129
ID ABU95828 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003036145-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 130
ID ABU91048 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003036154-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 131
ID ABU90141 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003036153-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 132
ID ABO09556 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003044931-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 133
ID ABO10828 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003036150-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 134
ID ABR70882 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003040069-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 135

ID ABU98263 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2002183493-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 136
ID ABU87490 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003022293-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 137
ID ABU91358 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003032128-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 138
ID ABU89268 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003036634-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 139
ID ABU84572 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003032116-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 140
ID ABR69662 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003032122-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 141
ID ABU80039 standard; protein; 266 AA.
DE Human PRO protein #5.
PN US2003036139-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 142
ID ABU82475 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2002183494-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 143
ID ABU92114 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003017476-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 144
ID ABU93308 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003017541-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 145
ID ABR70577 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003040076-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.

ID ABO09861 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003017543-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 146
ID ABO08946 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003036152-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 147
ID ABU96439 standard; protein; 266 AA.
DE Human PRO polypeptide #1.
PN US2003027993-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 148
ID ABU10820 standard; protein; 266 AA.
DE Human PRO polypeptide #6.
PN US2002123463-A1.
PD 05-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 149
ID ABU10514 standard; protein; 266 AA.
DE Human secreted/transmembrane protein #5.
PN US2002127584-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 150
ID ABU81572 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2002177164-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 151
ID ABU72109 standard; protein; 266 AA.
DE Human PRO polypeptide #1.
PN US2003023042-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 152
ID ABU95523 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003032115-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 153
ID ABU96732 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003032140-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 154
ID ABR70577 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003040076-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 155
ID ABO04928 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003008352-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 156
ID ABO08336 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003044922-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 157
ID ABU08511 standard; protein; 266 AA.
DE Human secreted and transmembrane polypeptide PRO180.
PN US2002197615-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 158
ID ABO34025 standard; protein; 266 AA.
DE Human PRO180 polypeptide.
PN US2003017981-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 159
ID ABO05543 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003032118-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 160
ID ABR73932 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003036135-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 161
ID ABR95524 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003054455-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 162
ID ABR80821 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003049741-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 163
ID ABR81126 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003049743-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 164
ID ABM00822 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.

PN US2003049769-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 165
ID ABR88424 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068743-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 166
ID ABM77245 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003054479-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 167
ID ABO28729 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003068685-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 168
ID ABO31474 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003068725-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 169
ID ABM07891 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068752-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 170
ID ABO40371 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003068682-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 171
ID ABO35796 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003068701-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 172
ID ABO43935 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003068755-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 173
ID ADA7762 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003073180-A1.

PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 174
ID ABM24730 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003104539-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 175
ID ABO02998 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003036131-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 176
ID ABR90254 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003040075-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 177
ID ABM17168 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003054459-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 178
ID ABR94914 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003044930-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 179
ID ABR95219 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003040071-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 180
ID ADB17059 standard; protein; 266 AA.
DE Human transmembrane PRO polypeptide (SeqID 2).
PN US2003050462-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 181
ID ABO21457 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003054471-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 182
ID ABR97721 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003064452-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 183
ID ABR87509 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068705-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 184
ID ABM77550 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003054473-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 185
ID ABM27780 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003064440-A1.
PD 03-APR-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 186
ID ABM06061 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068704-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 187
ID ABM03567 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068722-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 188
ID ABM35018 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003073183-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 189
ID ABM26255 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003104549-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 190
ID ABO48037 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003049749-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 191
ID ABR92779 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068462-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 192
ID ABO24540 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.

PN US2003065159-A1.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 193
ID ADA37534 standard; protein; 266 AA.
DE Human secreted/transmembrane protein PRO180.
PN US2003008297-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 194
ID ABM11551 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003064447-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 195
ID ABM02652 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003073184-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 196
ID ABM15948 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003064463-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 197
ID ABO27509 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003064451-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 198
ID ABM23000 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068721-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 199
ID ABM06976 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068699-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 200
ID ABM21070 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068707-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 201
ID ABM09416 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003073175-A1.

PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 202
ID ABO41286 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003068695-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 203
ID ABO36101 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003068703-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 204
ID ABO43630 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003068732-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 205
ID ABM76330 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003082717-A1.
PD 01-MAY-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 206
ID ABM76026 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003104548-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 207
ID ABM25645 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003104542-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 208
ID ABM25950 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003104543-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 209
ID ADA21220 standard; protein; 266 AA.
DE Human secreted/transmembrane polypeptide PRO180.
PN US2003054404-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 210
ID ABO03303 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003036127-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 211
ID ABO02388 standard; protein; 266 AA.

ID ABO39456 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003068776-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 231
ID ABM10331 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003069407-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 232
ID ABM11856 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003104555-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 233
ID ABO52002 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003049768-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 234
ID ABO52307 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003049771-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 235
ID ADA19864 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003069394-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 236
ID ABO23625 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003032134-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 237
ID ADB17247 standard; protein; 266 AA.
DE Human transmembrane PRO polypeptide (SeqID 2).
PN US2003050465-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 238
ID ADA17551 standard; protein; 266 AA.
DE Human PRO180 polypeptide.
PN US2003054987-A1.
PD 20-WAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 239
ID ABR97111 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003054481-A1.

PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 240
ID ABR86899 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003049778-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 241
ID ABM10941 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003049782-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 242
ID ABM28085 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003054476-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 243
ID ABO32084 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003068733-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 244
ID ABM15211 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068692-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 245
ID ABM06366 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068709-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 246
ID ABM04177 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068716-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 247
ID ABM22230 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068740-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 248
ID ABM07586 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068751-A1.
PD 10-APR-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 249
ID ABO40676 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003068684-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 250
ID ABM35323 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003073179-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 251
ID ABM33086 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003087374-A1.
PD 08-MAY-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 252
ID ABO52612 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003049773-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 253
ID ABO50172 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003049777-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 254
ID ABU99166 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003040055-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 255
ID ABO04218 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003036164-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 256
ID ABO05848 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003040074-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 257
ID ABM16388 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003054480-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
ID ADA27659 standard; protein; 266 AA.

DE Human secreted/transmembrane protein PRO180.
PN US2003054359-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 259
ID ABR97416 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003059885-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 260
ID ABR80516 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003049740-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 261
ID ABM01127 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003049770-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 262
ID ABR88729 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003073169-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 263
ID ABM13381 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003064457-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 264
ID ABM20765 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068711-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 265
ID ABO41896 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003049745-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 266
ID ABO42506 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003049751-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 267
ID ABM10026 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003067478-A1.
PD 10-APR-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 268
ID ABO39541 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003068773-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 269
ID ABM32781 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003073185-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 270
ID ABM22595 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003087373-A1.
PD 08-MAY-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 271
ID ABM74806 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003096353-A1.
PD 22-MAY-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 272
ID ADA79554 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003073173-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 273
ID ABR96196 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003054458-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 274
ID ABM02347 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003059886-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 275
ID ABR96289 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003049758-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 276
ID ABR86594 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003049772-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 277
ID ABM16558 standard; protein; 266 AA.

DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003064448-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 278
ID ABM29610 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003064456-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 279
ID ABO29034 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003068693-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 280
ID ABM23815 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068735-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 281
ID ABM23205 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068753-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 282
ID ABM21985 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068742-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 283
ID ABO37626 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003068756-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 284
ID ABM28390 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003082715-A1.
PD 01-MAY-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 285
ID ABM28695 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003082716-A1.
PD 01-MAY-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 286
ID ABM66339 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068737-A1.
PD 10-APR-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 287
ID ABM75721 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003104547-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 288
ID ABM34001 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003096359-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 289
ID ABM34306 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003100061-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 290
ID ABO20237 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003032125-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 291
ID ABO21152 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003054454-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 292
ID ABO22067 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003054477-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 293
ID ADA20036 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003052222-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 294
ID ABO34167 standard; protein; 266 AA.
DE Human secreted/transmembrane polypeptide PRO 180.
PN US2003060601-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 295
ID ABR96501 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003054460-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 296
ID ADA94239 standard; protein; 266 AA.
DE Human secreted/transmembrane protein PRO180.
PN US2003059832-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 297
ID ABR85679 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003049753-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 298
ID ABR99661 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003049763-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 299
ID ABM00212 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003073172-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 300
ID ABM00517 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003073172-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 301
ID ABO29644 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003068700-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 302
ID ABM23510 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068736-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 303
ID ABM29305 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068679-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 304
ID ABO38236 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003068767-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 305
ID ABO45536 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003073182-A1.

PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 306
ID ABM20460 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003104557-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 307
ID ADA81281 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003092121-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 308
ID ABO16574 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003027276-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 309
ID ABO18200 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003044920-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 310
ID ABO22627 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003027265-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 311
ID ABO22932 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003054461-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 312
ID ABR92474 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003064446-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 313
ID ABR81431 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003049744-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 314
ID ABM77855 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003049783-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 315
ID ABR99644 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003073171-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 316
ID ABM26560 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003032121-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 317
ID ABM13686 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003064458-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 318
ID ABO28424 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003064460-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 319
ID ABO30254 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003064464-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 320
ID ABM07281 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068702-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 321
ID ABM03872 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068734-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 322
ID ABO37016 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003068719-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 323
ID ABO41591 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003068729-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 324
ID ABO35186 standard; protein; 266 AA.
DE Human PRO polypeptide #5.

PN US2003068730-A1.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 344
ID ABM09111 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003073174-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 345
ID ABO39151 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003068775-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 346
ID ABM75416 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003104545-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 347
ID ABM25340 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003104541-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 348
ID ABM19850 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003104554-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 349
ID ABO46756 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003049762-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 350
ID ABO47061 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003049765-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 351
ID ADA83079 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003049752-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 352
ID ABR71492 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003032133-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 353
ID ABR72102 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003032136-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 354
ID ABR98441 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003036129-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 355
ID ABO06811 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003040053-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 356
ID ABR84764 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003040057-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 357
ID ABR73322 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003054467-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 358
ID ABR76416 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003044932-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 359
ID ABR73017 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003027270-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 360
ID ABM18083 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003054469-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 361
ID ABO20542 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003032126-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 362
ID ABO25285 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003054463-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;

Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 363
ID ABO25590 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003054466-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 364
ID ABR91999 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003059879-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 365
ID ADA92585 standard; protein; 266 AA.
DE Human secreted/transmembrane protein PRO180.
PN US2003060407-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 366
ID ABR79906 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003049738-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 367
ID ABO32853 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003064453-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 368
ID ABO32853 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003064453-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 369
ID ABO30559 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003064466-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 370
ID ABO30864 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003064468-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 371
ID ABO30864 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003064468-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 372
ID ABR29915 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068760-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 373
ID ABO45841 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003049754-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 374
ID ABO45841 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003049754-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 375
ID ABO42201 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003049748-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 376
ID ABO42201 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003049748-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 377
ID ABO37931 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003068765-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 378
ID ABO45841 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003049754-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 379
ID ABO45841 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068688-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 380
ID ADB20122 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003082767-A1.
PD 01-MAY-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 381
ID ABR19545 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003104552-A1.

PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 382
ID ABO49257 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003049774-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 383
ID ABO49562 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003049775-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 384
ID ADA78374 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003073181-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 385
ID ABR88119 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068720-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 386
ID ADA00333 standard; protein; 266 AA.
DE Human secreted/transmembrane polypeptide PRO 180.
PN US2003027992-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 387
ID ABM26865 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068739-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 388
ID ABM03262 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068763-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 389
ID ABO39761 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003068689-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 390
ID ABO49867 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003049776-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 391
ID ABO50782 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003049780-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 392
ID ABO05238 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003036126-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 393
ID ABR74542 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003044924-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 394
ID ABR77021 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003044927-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 395
ID ABM17778 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003040072-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 396
ID ABR95829 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003040073-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 397
ID ABO21762 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003054475-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 398
ID ABO19932 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003032124-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 399
ID ABO24235 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003064467-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 400
ID ABR85984 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003049759-A1.

PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 401
ID ABM10636 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003064455-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 402
ID ABM76635 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003054465-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 403
ID ABR89339 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003073170-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 404
ID ABM12466 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003073176-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 405
ID ABM05756 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068717-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 406
ID ABO34881 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003068728-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 407
ID ABM02957 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068764-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 408
ID ABM18935 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003104550-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 409
ID ABM19240 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003104551-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 410
ID ABO46451 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003049761-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 411
ID ABO48952 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003049757-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 412
ID ABR68995 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003027273-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 413
ID ABR89034 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003036119-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 414
ID ABR72407 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003036120-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 415
ID ABR74237 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003036161-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 416
ID ABO18505 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003044921-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 417
ID ABR80211 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003049739-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 418
ID ABM01432 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003059882-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 419
ID ABM02042 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.

PN US2003059884-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 420
ID ABR87204 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068687-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 421
ID ABM12771 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003073186-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 422
ID ABM30525 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003064443-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 423
ID ABM24425 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003064444-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 424
ID ABO29339 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003068697-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 425
ID ABO31169 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003068710-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 426
ID ABM14296 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068686-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 427
ID ABM09721 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003073178-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 428
ID ABO38846 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003068774-A1.

PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 429
ID ABM34611 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003104538-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 430
ID ABO51087 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003049781-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 431
ID ABO03913 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003036158-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 432
ID ABO10383 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003036151-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 433
ID ABO53111 standard; protein; 266 AA.
DE Human secreted/transmembrane protein PRO180.
PN US2003044806-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 434
ID ABR77626 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003040067-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 435
ID ABR78836 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003054456-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 436
ID ABO23930 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003054482-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 437
ID ABR93694 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003054457-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 438
ID ABM01737 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.

PN US2003059883-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 7; Length 266;
Pred. No. 5e-149;
RESULT 439
ID ABM78160 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003049764-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 7; Length 266;
Pred. No. 5e-149;
RESULT 440
ID ABR89949 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003073177-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 7; Length 266;
Pred. No. 5e-149;
RESULT 441
ID ADA22146 standard; protein; 266 AA.
DE Human secreted/transmembrane polypeptide PRO180.
PN US2003040473-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 7; Length 266;
Pred. No. 5e-149;
RESULT 442
ID ABM27475 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003064442-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 7; Length 266;
Pred. No. 5e-149;
RESULT 443
ID ABM13076 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003064450-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 7; Length 266;
Pred. No. 5e-149;
RESULT 444
ID ABO31779 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003068731-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 7; Length 266;
Pred. No. 5e-149;
RESULT 445
ID ABM13991 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068683-A1.
PD 10-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 7; Length 266;
Pred. No. 5e-149;
RESULT 446
ID ABM08196 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068754-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 7; Length 266;
Pred. No. 5e-149;
RESULT 447
ID ABO40066 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003068681-A1.
PD 10-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 7; Length 266;
Pred. No. 5e-149;
RESULT 448
ID ABM74501 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003096351-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 7; Length 266;
Pred. No. 5e-149;
RESULT 449
ID ABM33696 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003096358-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 7; Length 266;
Pred. No. 5e-149;
RESULT 450
ID ABM20155 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003104556-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 7; Length 266;
Pred. No. 5e-149;
RESULT 451
ID ABO48647 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003049756-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 7; Length 266;
Pred. No. 5e-149;
RESULT 452
ID ABO22481 standard; protein; 266 AA.
DE Human secreted/transmembrane protein PRO180.
PN US2003017982-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 7; Length 266;
Pred. No. 5e-149;
RESULT 453
ID ABR72712 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003036122-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 7; Length 266;
Pred. No. 5e-149;
RESULT 454
ID ABO15354 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003036121-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 7; Length 266;
Pred. No. 5e-149;
RESULT 455
ID ABR85069 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003040085-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 7; Length 266;
Pred. No. 5e-149;
RESULT 456
ID ABO15049 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003044919-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 7; Length 266;
Pred. No. 5e-149;
RESULT 457
ID ABO17184 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003040077-A1.

DE Novel human secreted and transmembrane protein PRO180.
PN US2003049735-A1.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 477
ID ADB96031 standard; protein; 266 AA.
DE Human PRO polypeptide #6.
PN US2003054403-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 478
ID ABM31745 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068680-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 479
ID ABM31135 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068762-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 480
ID ADB85753 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003054472-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 481
ID ARM32050 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068708-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 482
ID ABM32355 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068713-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 483
ID ADB68254 standard; protein; 266 AA.
DE Human PRO180 protein.
PN US2003065161-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 484
ID ADB68061 standard; protein; 266 AA.
DE Human PRO180 protein.
PN US2003060600-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 485
ID ABM31440 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068761-A1.
PD 10-APR-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 486
ID ABM30830 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068771-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 487
ID ADB90878 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003083473-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 488
ID ADC57503 standard; protein; 266 AA.
DE Human PRO polypeptide #6.
PN US2003027754-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 489
ID ADC54867 standard; protein; 266 AA.
DE Human PRO polypeptide #6.
PN US2003045463-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 490
ID ADC11734 standard; protein; 266 AA.
DE Human secreted/transmembrane protein PRO180.
PN US2003049681-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 491
ID ADC06958 standard; protein; 266 AA.
DE Human PRO180 protein.
PN US2003060602-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 492
ID ADC56156 standard; protein; 266 AA.
DE Human PRO polypeptide #6.
PN US2003064375-A1.
PD 03-APR-2003.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 493
ID ADC17137 standard; protein; 266 AA.
DE Mammalian PRO polypeptide (SeqID 2).
PN US2003065143-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 494
ID ADC07211 standard; protein; 266 AA.
DE Human secreted/transmembrane protein PRO180.
PN US2003068647-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 495
ID ADC11201 standard; protein; 266 AA.
DE Human secreted/transmembrane protein PRO180.

PN US2003069403-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 496
ID ADC14835 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003073208-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 497
ID ADC52330 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003138882-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 498
ID ADC14323 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003082546-A1.
PD 01-MAY-2003.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 499
ID ADD07855 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003068623-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 500
ID ADC81680 standard; protein; 266 AA.
DE Human PRO polypeptide #6.
PN US2003083461-A1.
PD 01-MAY-2003.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 501
ID ADD07322 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2002193299-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 502
ID ADC82213 standard; protein; 266 AA.
DE Human PRO polypeptide #6.
PN US2003059833-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 503
ID ADD05483 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003087376-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 504
ID ADC78249 standard; protein; 266 AA.
DE Human secreted protein SEQ ID NO:56.
PN WO2003072761-A1.
PD 04-SEP-2003.
PA (HUWA-) HUMAN GENOME SCI INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 505

ID ADB08393 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003073090-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 506
ID ADB06642 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2002193300-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 507
ID ADC82889 standard; protein; 266 AA.
DE Human PRO polypeptide #6.
PN US2003059783-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 508
ID ADB54996 standard; protein; 266 AA.
DE Human PRO polypeptide #6.
PN US2003077593-A1.
PD 24-APR-2003.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 509
ID ADB36006 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003105298-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 510
ID ADB55954 standard; protein; 266 AA.
DE Human PRO polypeptide #6.
PN US2003077594-A1.
PD 24-APR-2003.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 511
ID ADB54392 standard; protein; 266 AA.
DE Human PRO polypeptide #6.
PN US2002132253-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 512
ID ADB26546 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003087304-A1.
PD 08-MAY-2003.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 513
ID ADB26013 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003087305-A1.
PD 08-MAY-2003.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 514
ID ADF66950 standard; protein; 266 AA.
DE Human PRO180 amino acid sequence SEQ ID NO:23.
PN US2002198148-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;

RESULT 515
ID ADG01007 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003078387-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 516
ID ADG08560 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180793-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 517
ID ADG02478 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003207397-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 518
ID ADG01185 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003207399-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 519
ID ADF95360 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003207399-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 520
ID ADF95181 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180795-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 521
ID ADG12175 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003207392-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 522
ID ADH24034 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180918-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 523
ID ADH34060 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180858-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 524
ID ADH29893 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180859-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 525
ID ADH23864 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180919-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 526
ID ADH08935 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003207395-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 527
ID ADG85268 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180904-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 528
ID ADH24544 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180907-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 529
ID ADH37400 standard; protein; 266 AA.
DE Human secreted and transmembrane protein PRO180.
PN US2003181646-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 530
ID ADH01989 standard; protein; 266 AA.
DE Human PRO polypeptide #1.
PN US2003180837-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 531
ID ADH37570 standard; protein; 266 AA.
DE Human secreted and transmembrane protein PRO180.
PN US2003181648-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 532
ID ADG85608 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180905-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 533
ID ADH24204 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180905-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;

PN US2003180914-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 534
ID ADH38498 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181643-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 535
ID ADG83619 standard; protein; 266 AA.
DE Human PRO polypeptide #1.
PN US2003180794-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 536
ID ADH29427 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180860-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 537
ID ADH27543 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180906-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 538
ID ADH37740 standard; protein; 266 AA.
DE Human secreted and transmembrane protein PRO180.
PN US2003181647-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 539
ID ADH37917 standard; protein; 266 AA.
DE Human secreted and transmembrane protein PRO180.
PN US2003181649-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 540
ID ADH57337 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180920-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 541
ID ADH53479 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181636-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 542
ID ADH53649 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181641-A1.

PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 543
ID ADH51985 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181638-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 544
ID ADH49840 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181639-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 545
ID ADI25350 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181696-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 546
ID ADH90143 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181698-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 547
ID ADI25520 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181669-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 548
ID ADH97694 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181672-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 549
ID ADI35204 standard; protein; 266 AA.
DE Human PRO polypeptide #6.
PN US2003050457-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 550
ID ADI03542 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181656-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 551
ID ADI11899 standard; protein; 266 AA.
DE Human PRO polypeptide #1.
PN US2003181686-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 552
ID ADH89973 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181697-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 553
ID ADH99696 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003049682-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 554
ID ADH98374 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181707-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 555
ID ADI11049 standard; protein; 266 AA.
DE Human PRO polypeptide #1.
PN US2003181682-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 556
ID ADI11559 standard; protein; 266 AA.
DE Human PRO polypeptide #1.
PN US2003181684-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 557
ID ADH98204 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181709-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 558
ID ADH98544 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181708-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 559
ID ADH98034 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181673-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 560
ID ADI05022 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180848-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;

RESULT 561
ID ADI03372 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181654-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 562
ID ADI04767 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181657-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 563
ID ADH78221 standard; protein; 266 AA.
DE Human PRO polypeptide #1.
PN US2003181658-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 564
ID ADI19565 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181676-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 565
ID ADH90313 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181699-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 566
ID ADI03032 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181653-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 567
ID ADH77881 standard; protein; 266 AA.
DE Human PRO polypeptide #1.
PN US2003181666-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 568
ID ADH97864 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181674-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 569
ID ADI01249 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003190669-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 570
ID ADI01249 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003190669-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;

ID ADI01944 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181652-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 571
ID ADI03202 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181655-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 572
ID ADI11389 standard; protein; 266 AA.
DE Human PRO polypeptide #1.
PN US2003181681-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 573
ID ADI02291 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181650-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 574
ID ADI11729 standard; protein; 266 AA.
DE Human PRO polypeptide #1.
PN US2003181685-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 575
ID ADI05366 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003190716-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 576
ID ADH79438 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003191290-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 577
ID ADI19395 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181675-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 578
ID ADI05196 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181677-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
ID ADH79608 standard; protein; 266 AA.

DE Novel human secreted and transmembrane protein PRO180.
PN US2003191288-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 580
ID ADI01434 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181678-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 581
ID ADI01604 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181679-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 582
ID ADI01774 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181680-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 583
ID ADH79778 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003191289-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 584
ID ADI04596 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003171550-A1.
PD 11-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 585
ID ADI02732 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181651-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 586
ID ADH78051 standard; protein; 266 AA.
DE Human PRO polypeptide #1.
PN US2003181667-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 587
ID ADI25690 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181670-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 588
ID ADI25860 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.

PN	US2003181671-A1.	Query Match	100.0%;	Score 1392;	DB 8;	Length 266;
PD	25-SEP-2003.	Best Local Similarity	100.0%;	Pred. No. 5e-149;		
PA	(GETH) GENENTECH INC.	RESULT 598				
DE	ADP35149 standard; protein; 266 AA.	Query Match	100.0%;	Score 1392;	DB 7;	Length 266;
ID	ADP35149 standard; protein; 266 AA.	Best Local Similarity	100.0%;	Pred. No. 5e-149;		
DE	Human PRO180 polypeptide.	Query Match	100.0%;	Score 1392;	DB 8;	Length 266;
PN	US2003194760-A1.	Best Local Similarity	100.0%;	Pred. No. 5e-149;		
PD	16-OCT-2003.	RESULT 599				
PA	(GETH) GENENTECH INC.	Query Match	100.0%;	Score 1392;	DB 8;	Length 266;
DE	ADG11399 standard; protein; 266 AA.	Best Local Similarity	100.0%;	Pred. No. 5e-149;		
ID	ADG11399 standard; protein; 266 AA.	Query Match	100.0%;	Score 1392;	DB 8;	Length 266;
DE	Human PRO180 polypeptide.	Best Local Similarity	100.0%;	Pred. No. 5e-149;		
PN	US2003228655-A1.	Query Match	100.0%;	Score 1392;	DB 8;	Length 266;
PD	11-DEC-2003.	Best Local Similarity	100.0%;	Pred. No. 5e-149;		
PA	(GETH) GENENTECH INC.	Query Match	100.0%;	Score 1392;	DB 8;	Length 266;
DE	Novel human secreted and transmembrane protein PRO180.	Best Local Similarity	100.0%;	Pred. No. 5e-149;		
PN	US2003215909-A1.	Query Match	100.0%;	Score 1392;	DB 8;	Length 266;
PD	20-NOV-2003.	Best Local Similarity	100.0%;	Pred. No. 5e-149;		
PA	(GETH) GENENTECH INC.	Query Match	100.0%;	Score 1392;	DB 8;	Length 266;
DE	ADG04243 standard; protein; 266 AA.	Best Local Similarity	100.0%;	Pred. No. 5e-149;		
ID	ADG04243 standard; protein; 266 AA.	Query Match	100.0%;	Score 1392;	DB 8;	Length 266;
DE	Novel human secreted and transmembrane protein PRO180.	Best Local Similarity	100.0%;	Pred. No. 5e-149;		
PN	US2003215912-A1.	Query Match	100.0%;	Score 1392;	DB 8;	Length 266;
PD	20-NOV-2003.	Best Local Similarity	100.0%;	Pred. No. 5e-149;		
PA	(GETH) GENENTECH INC.	Query Match	100.0%;	Score 1392;	DB 8;	Length 266;
DE	ADG00403 standard; protein; 266 AA.	Best Local Similarity	100.0%;	Pred. No. 5e-149;		
ID	ADG00403 standard; protein; 266 AA.	Query Match	100.0%;	Score 1392;	DB 8;	Length 266;
DE	Novel human secreted and transmembrane protein PRO180.	Best Local Similarity	100.0%;	Pred. No. 5e-149;		
PN	US2003215911-A1.	Query Match	100.0%;	Score 1392;	DB 8;	Length 266;
PD	20-NOV-2003.	Best Local Similarity	100.0%;	Pred. No. 5e-149;		
PA	(GETH) GENENTECH INC.	Query Match	100.0%;	Score 1392;	DB 8;	Length 266;
DE	ADH06572 standard; protein; 266 AA.	Best Local Similarity	100.0%;	Pred. No. 5e-149;		
ID	ADH06572 standard; protein; 266 AA.	Query Match	100.0%;	Score 1392;	DB 8;	Length 266;
DE	Novel human secreted and transmembrane protein PRO180.	Best Local Similarity	100.0%;	Pred. No. 5e-149;		
PN	US2003180852-A1.	Query Match	100.0%;	Score 1392;	DB 8;	Length 266;
PD	25-SEP-2003.	Best Local Similarity	100.0%;	Pred. No. 5e-149;		
PA	(GETH) GENENTECH INC.	Query Match	100.0%;	Score 1392;	DB 8;	Length 266;
DE	ADH06402 standard; protein; 266 AA.	Best Local Similarity	100.0%;	Pred. No. 5e-149;		
ID	ADH06402 standard; protein; 266 AA.	Query Match	100.0%;	Score 1392;	DB 8;	Length 266;
DE	Novel human secreted and transmembrane protein PRO180.	Best Local Similarity	100.0%;	Pred. No. 5e-149;		
PN	US2003180853-A1.	Query Match	100.0%;	Score 1392;	DB 8;	Length 266;
PD	25-SEP-2003.	Best Local Similarity	100.0%;	Pred. No. 5e-149;		
PA	(GETH) GENENTECH INC.	Query Match	100.0%;	Score 1392;	DB 8;	Length 266;
DE	ADG68823 standard; protein; 266 AA.	Best Local Similarity	100.0%;	Pred. No. 5e-149;		
ID	ADG68823 standard; protein; 266 AA.	Query Match	100.0%;	Score 1392;	DB 8;	Length 266;
DE	Novel human secreted and transmembrane protein PRO180.	Best Local Similarity	100.0%;	Pred. No. 5e-149;		
PN	US2003180855-A1.	Query Match	100.0%;	Score 1392;	DB 8;	Length 266;
PD	25-SEP-2003.	Best Local Similarity	100.0%;	Pred. No. 5e-149;		
PA	(GETH) GENENTECH INC.	Query Match	100.0%;	Score 1392;	DB 8;	Length 266;
DE	ADH27713 standard; protein; 266 AA.	Best Local Similarity	100.0%;	Pred. No. 5e-149;		
ID	ADH27713 standard; protein; 266 AA.	Query Match	100.0%;	Score 1392;	DB 8;	Length 266;
DE	Novel human secreted and transmembrane protein PRO180.	Best Local Similarity	100.0%;	Pred. No. 5e-149;		
PN	US2003180912-A1.	Query Match	100.0%;	Score 1392;	DB 8;	Length 266;
PD	25-SEP-2003.	Best Local Similarity	100.0%;	Pred. No. 5e-149;		
PA	(GETH) GENENTECH INC.	Query Match	100.0%;	Score 1392;	DB 8;	Length 266;
DE	ADH74759 standard; protein; 266 AA.	Best Local Similarity	100.0%;	Pred. No. 5e-149;		
ID	ADH74759 standard; protein; 266 AA.	Query Match	100.0%;	Score 1392;	DB 8;	Length 266;

ID ADH25054 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180913-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 608
ID ADH33686 standard; protein; 266 AA.
DE Human PRO polypeptide #1.
PN US2003181645-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 609
ID ADG82659 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003215910-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 610
ID ADH02329 standard; protein; 266 AA.
DE Human PRO polypeptide #1.
PN US2003180839-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 611
ID ADH07936 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180845-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 612
ID ADG69333 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180846-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 613
ID ADH39154 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180917-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 614
ID ADH25940 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003068770-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 615
ID ADG83894 standard; protein; 266 AA.
DE Human PRO polypeptide #1.
PN US2003180842-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
ID ADH19269 standard; protein; 266 AA.

DE Human secreted/transmembrane protein PRO180.
PN US2003228656-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 617
ID ADG85438 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003166848-A1.
PD 04-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 618
ID ADH06232 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180854-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 619
ID ADH30063 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180856-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 620
ID ADH24374 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180910-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 621
ID ADH32909 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003068768-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 622
ID ADG69503 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180844-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 623
ID ADH07766 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180851-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 624
ID ADG85778 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180861-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 625
ID ADH39324 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.

PN US2003180916-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 626
ID ADH33516 standard; protein; 266 AA.
DE Human PRO polypeptide #1.
PN US2003181637-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 627
ID ADH33856 standard; protein; 266 AA.
DE Human PRO polypeptide #1.
PN US2003181644-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 628
ID ADH01066 standard; protein; 266 AA.
DE Human PRO polypeptide #1.
PN US2003180838-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 629
ID ADG69673 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180843-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 630
ID ADH20762 standard; protein; 266 AA.
DE Human secreted/transmembrane protein PRO180.
PN US2003224358-A1.
PD 04-DEC-2003.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 631
ID ADH02159 standard; protein; 266 AA.
DE Human PRO polypeptide #1.
PN US2003180841-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 632
ID ADG69163 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180847-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 633
ID ADG85948 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180862-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 634
ID ADH24884 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180909-A1.
PD 25-SEP-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 635
ID ADH39501 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180915-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 636
ID ADH19802 standard; protein; 266 AA.
DE Human secreted/transmembrane protein PRO180.
PN US2003219856-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 637
ID ADH02499 standard; protein; 266 AA.
DE Human PRO polypeptide #1.
PN US2003180840-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 638
ID ADG68993 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180849-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 639
ID ADH07596 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180850-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 640
ID ADG86118 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180863-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 641
ID ADH24714 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180908-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 642
ID ADH25762 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180911-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 643
ID ADH38328 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180922-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 643
ID ADH38328 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180922-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 644
ID ADH57167 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181642-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 645
ID ADH52155 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180921-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 646
ID ADH49521 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180857-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 647
ID ADH90483 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181700-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 648
ID ADI1219 standard; protein; 266 AA.
DE Human PRO polypeptide #1.
PN US2003181683-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 649
ID ADH9884 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003190698-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 650
ID ADI02114 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003190699-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 651
ID ADH90653 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181701-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 652
ID ADJ54648 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2004023321-A1.
PD 05-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;

Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 653
ID ADJ98528 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003187197-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 654
ID ADJ98698 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003187228-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 655
ID ADH78857 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181703-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 656
ID ADJ99091 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003186408-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 657
ID ADJ99261 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003187196-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 658
ID ADJ98879 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003187242-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 659
ID ADH79027 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181702-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 660
ID ADK00887 standard; protein; 266 AA.
DE Human PRO polypeptide #1.
PN US2003186407-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 661
ID ADK14408 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003187229-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;

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RESULT 662
ID ADJ64419 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2004038337-A1.
PD 26-FEB-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 663
ID ADM31315 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2004048334-A1.
PD 11-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 664
ID ADM36362 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2004053358-A1.
PD 18-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 665
ID ADM40167 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2004048335-A1.
PD 11-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 666
ID ADM80857 standard; protein; 266 AA.
DE Human PRO polypeptide #1.
PN US2004058411-A1.
PD 25-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 667
ID ADN60677 standard; protein; 266 AA.
DE Human secreted polypeptide #9.
PN US2004038277-A1.
PD 26-FEB-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 668
ID ADN37775 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2004091959-A1.
PD 13-MAY-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 669
ID ADY77697 standard; protein; 266 AA.
DE Neoplastic disease detection protein PRO180.
PN US2005059102-A1.
PD 17-MAR-2005.
PA (EATO/) EATON D L.
PA (FILV/) FILVAROFF E.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI J C.
PA (GURN/) GURNEY A L.
PA (WATA/) WATANABE C K.
PA (WOOD/) WOOD W I.
Query Match 100.0%; Score 1392; DB 9; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 670
ID AEA38350 standard; protein; 266 AA.
DE Human secreted/transmembrane protein cDNA, #73.
PN US2005112725-A1.
PD 26-MAY-2005.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 9; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 671
ID AED11495 standard; protein; 266 AA.
DE Human gene 26 encoded secreted protein HCP191, SEQ ID NO: 56.
PN US2005214786-A1.
PD 29-SEP-2005.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 100.0%; Score 1392; DB 9; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 672
ID AED50005 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2005163766-A1.
PD 28-JUL-2005.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 9; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 673
ID AEF12528 standard; protein; 266 AA.
DE Human PRO180 protein SEQ ID NO:2.
PN US2006008901-A1.
PD 12-JAN-2006.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 10; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 674
ID AEF74217 standard; protein; 266 AA.
DE Human PRO180 protein SEQ ID NO:2.
PN US2005260647-A1.
PD 24-NOV-2005.
PA (EATO/) EATON D L.
PA (FILV/) FILVAROFF E.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI J C.
PA (GURN/) GURNEY A L.
PA (WATA/) WATANABE C K.
PA (WOOD/) WOOD W L.
Query Match 100.0%; Score 1392; DB 10; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 675
ID AAY27575 standard; protein; 267 AA.
DE Human secreted protein encoded by gene No. 9.
PN WO9924836-A1.
PD 20-MAY-1999.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 100.0%; Score 1392; DB 2; Length 267;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 676
ID ADG78386 standard; protein; 267 AA.
DE Human secreted protein #9.
PN US2003211472-A1.
PD 13-NOV-2003.
PA (FENG/) FENG P.
PA (RUBE/) RUBEN S M.
PA (ROSE/) ROSEN C A.
PA (EBNE/) EBNER R.
PA (OLSE/) OLSEN H S.
PA (NIJ/) NI J.
PA (WEI/) WEI Y.
PA (SOPP/) SOPPET D R.
PA (MOOR/) MOORE P A.
PA (KYAW/) KYAW H.
PA (LAF/) LAFLEUR D W.
PA (SHI/) SHI Y.
PA (JANA/) JANAT F.
PA (ENDR/) ENDRESS G A.
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PA (CART/) CARTER K C.
Query Match 100.0%; Score 1392; DB 8; Length 267;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 677
ID ABB12041 standard; peptide; 275 AA.
DE Human secreted protein homologue, SEQ ID NO:2411.
PN WO200157188-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 100.0%; Score 1392; DB 4; Length 275;
Best Local Similarity 100.0%; Pred. No. 5.2e-149;
RESULT 678
ID AAM41354 standard; protein; 275 AA.
DE Human polypeptide SEQ ID NO 6285.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 100.0%; Score 1392; DB 4; Length 275;
Best Local Similarity 100.0%; Pred. No. 5.2e-149;
RESULT 679
ID AAB87526 standard; protein; 266 AA.
DE Human PRO180.
PN WO200116318-A2.
PD 08-MAR-2001.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1390; DB 4; Length 266;
Best Local Similarity 99.6%; Pred. No. 8.4e-149;
RESULT 680
ID AAY36185 standard; protein; 267 AA.
DE Human secreted protein #57.
PN WO9925825-A2.
PD 27-MAY-1999.
PA (GEST) GENSET.
Query Match 99.7%; Score 1388; DB 2; Length 267;
Best Local Similarity 99.6%; Pred. No. 1.4e-148;
RESULT 681
ID ADJ46037 standard; protein; 267 AA.
DE Novel human secreted protein-related protein sequence SeqID190.
PN US2003144490-A1.
PD 31-JUL-2003.
PA (EDWA/) EDWARDS J D M.
PA (DUCL/) DUCLERT A.
PA (BOUG/) BOUGUELERET L.
Query Match 99.7%; Score 1388; DB 7; Length 267;
Best Local Similarity 99.6%; Pred. No. 1.4e-148;
RESULT 682
ID ADP19446 standard; protein; 267 AA.
DE Human secreted polypeptide #297.
PN US2004110939-A1.
PD 10-JUN-2004.
PA (GEST) GENSET SA.
Query Match 99.7%; Score 1388; DB 8; Length 267;
Best Local Similarity 99.6%; Pred. No. 1.4e-148;
RESULT 683
ID AAY29866 standard; protein; 208 AA.
DE Human secreted protein clone pe318_4.
PN WO9946287-A1.
PD 16-SEP-1999.
PA (GENY) GENETICS INST INC.
Query Match 77.4%; Score 1078; DB 2; Length 208;
Best Local Similarity 100.0%; Pred. No. 1.6e-113;
RESULT 684
ID ABP75476 standard; protein; 166 AA.
DE Human secretory polypeptide SPTM SEQ ID NO 660.
PN WO200283876-A2.
PD 24-OCT-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 58.6%; Score 816; DB 6; Length 166;
Best Local Similarity 93.4%; Pred. No. 6.8e-84;
RESULT 685
ID AAB88330 standard; protein; 136 AA.
DE Human membrane or secretory protein clone PSEC0031.
PN EP1067182-A2.

PD 10-JAN-2001.
PA (HELI-) HELIX RES INST.
Query Match 52.1%; Score 725; DB 4; Length 136;
Best Local Similarity 100.0%; Pred. No. 1.1e-73;
RESULT 686
ID ADY63025 standard; protein; 136 AA.
DE Human clone PSEC0031 protein, SEQ ID 28.
PN EP1514933-A1.
PD 16-MAR-2005.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 52.1%; Score 725; DB 9; Length 136;
Best Local Similarity 100.0%; Pred. No. 1.1e-73;
RESULT 687
ID AAY36138 standard; protein; 172 AA.
DE Human secreted protein #10.
PN WO9925825-A2.
PD 27-MAY-1999.
PA (GEST) GENSET.
Query Match 42.8%; Score 595.5; DB 2; Length 172;
Best Local Similarity 79.4%; Pred. No. 8e-59;
RESULT 688
ID ADJ45943 standard; protein; 172 AA.
DE Novel human secreted protein-related protein sequence SeqID96.
PN US2003144490-A1.
PD 31-JUL-2003.
PA (EDWA/) EDWARDS J D M.
PA (DUCL/) DUCLERT A.
PA (BOUG/) BOUGUELERET L.
Query Match 42.8%; Score 595.5; DB 7; Length 172;
Best Local Similarity 79.4%; Pred. No. 8e-59;
RESULT 689
ID ADM04182 standard; protein; 238 AA.
DE Human protein of the invention SEQ ID NO:2867.
PN EP1347046-A1.
PD 24-SEP-2003.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 34.9%; Score 486.5; DB 7; Length 238;
Best Local Similarity 38.6%; Pred. No. 3e-46;
RESULT 690
ID AEC87112 standard; protein; 238 AA.
DE Human cDNA clone protein BRCC20101230, SEQ ID 2867.
PN EP1580263-A1.
PD 28-SEP-2005.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 34.9%; Score 486.5; DB 9; Length 238;
Best Local Similarity 38.6%; Pred. No. 3e-46;
RESULT 691
ID AAE26425 standard; protein; 231 AA.
DE Human transmembrane protein (TMP)-11 protein.
PN WO200234783-A2.
PD 02-MAY-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 34.5%; Score 480.5; DB 5; Length 231;
Best Local Similarity 38.7%; Pred. No. 1.4e-45;
RESULT 692
ID ADK70499 standard; protein; 231 AA.
DE Respiratory disease differentially expressed protein #65.
PN WO2003101283-A2.
PD 11-DEC-2003.
PA (INCY-) INCYTE CORP.
Query Match 34.5%; Score 480.5; DB 8; Length 231;
Best Local Similarity 38.7%; Pred. No. 1.4e-45;
RESULT 693
ID AAE05342 standard; protein; 238 AA.
DE Mouse secreted protein #1.
PN WO200148192-A1.
PD 05-JUL-2001.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 34.4%; Score 479.5; DB 4; Length 238;
Best Local Similarity 37.3%; Pred. No. 1.9e-45;
RESULT 694
ID ABO00865 standard; protein; 246 AA.
DE Polypeptide encoded by novel human contig #116.

PN WO2003023013-A2.
PD 20-MAR-2003.
PA (HYSE-) HYSEQ INC.
Query Match 33.2%; Score 461.5; DB 6; Length 246;
Best Local Similarity 39.3%; Pred. No. 2.2e-43;
RESULT 695
ID ABB60356 standard; protein; 246 AA.
DE Drosoophila melanogaster polypeptide SEQ ID NO 7860.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 26.0%; Score 361.5; DB 4; Length 246;
Best Local Similarity 33.6%; Pred. No. 4.9e-32;
RESULT 696
ID AAY36219 standard; protein; 69 AA.
DE Human secreted protein #91.
PN WO9925825-A2.
PD 27-MAY-1999.
PA (GEST) GENSET.
Query Match 25.7%; Score 358; DB 2; Length 69;
Best Local Similarity 100.0%; Pred. No. 2.1e-32;
RESULT 697
ID AAY36172 standard; protein; 69 AA.
DE Human secreted protein #44.
PN WO9925825-A2.
PD 27-MAY-1999.
PA (GEST) GENSET.
Query Match 25.7%; Score 358; DB 2; Length 69;
Best Local Similarity 100.0%; Pred. No. 2.1e-32;
RESULT 698
ID ADJ46071 standard; protein; 69 AA.
DE Novel human secreted protein-related protein sequence SeqID224.
PN US2003144490-A1.
PD 31-JUL-2003.
PA (EDWA/) EDWARDS J D M.
PA (DUCL/) DUCLERT A.
PA (BOUG/) BOUGUELERET L.
Query Match 25.7%; Score 358; DB 7; Length 69;
Best Local Similarity 100.0%; Pred. No. 2.1e-32;
RESULT 699
ID ADJ45977 standard; protein; 69 AA.
DE Novel human secreted protein-related protein sequence SeqID130.
PN US2003144490-A1.
PD 31-JUL-2003.
PA (EDWA/) EDWARDS J D M.
PA (DUCL/) DUCLERT A.
PA (BOUG/) BOUGUELERET L.
Query Match 25.7%; Score 358; DB 7; Length 69;
Best Local Similarity 100.0%; Pred. No. 2.1e-32;
RESULT 700
ID ADP19480 standard; protein; 69 AA.
DE Human secreted polypeptide #331.
PN US2004110939-A1.
PD 10-JUN-2004.
PA (GEST) GENSET SA.
Query Match 25.7%; Score 358; DB 7; Length 69;
Best Local Similarity 100.0%; Pred. No. 2.1e-32;
RESULT 701
ID ABB97776 standard; protein; 85 AA.
DE Human secretory polypeptide (SPTM) 28.
PN WO200220756-A2.
PD 14-MAR-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 25.6%; Score 356; DB 5; Length 85;
Best Local Similarity 86.1%; Pred. No. 4.8e-32;

RESULT 703
ID AAY04148 standard; protein; 69 AA.
DE Human 5' EST secreted protein SEQ ID NO:19.
PN WO9906439-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.
Query Match 25.3%; Score 352; DB 2; Length 69;
Best Local Similarity 98.5%; Pred. No. 1e-31;
RESULT 704
ID AAW93616 standard; protein; 69 AA.
DE Human 5' EST secreted protein clone 58-34-2-E7-FL2.
PN WO9906551-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.
Query Match 25.3%; Score 352; DB 2; Length 69;
Best Local Similarity 98.5%; Pred. No. 1e-31;
RESULT 705
ID AAY04166 standard; protein; 69 AA.
DE Human 5' EST secreted protein SEQ ID NO:19.
PN WO9906548-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.
Query Match 25.3%; Score 352; DB 2; Length 69;
Best Local Similarity 98.5%; Pred. No. 1e-31;
RESULT 706
ID AAY35882 standard; protein; 69 AA.
DE Extended human secreted protein sequence, SEQ ID NO. 19.
PN WO9931236-A2.
PD 24-JUN-1999.
PA (GEST) GENSET.
Query Match 25.3%; Score 352; DB 2; Length 69;
Best Local Similarity 98.5%; Pred. No. 1e-31;
RESULT 707
ID AAY59645 standard; protein; 69 AA.
DE Secreted protein extended EST protein sequence #2.
PN WO9940189-A2.
PD 12-AUG-1999.
PA (GEST) GENSET.
Query Match 25.3%; Score 352; DB 2; Length 69;
Best Local Similarity 98.5%; Pred. No. 1e-31;
RESULT 708
ID AAY01590 standard; protein; 69 AA.
DE Secreted protein encoded by an extended 5' EST cDNA sequence.
PN WO9906554-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.
Query Match 25.3%; Score 352; DB 2; Length 69;
Best Local Similarity 98.5%; Pred. No. 1e-31;
RESULT 709
ID AAY12982 standard; protein; 69 AA.
DE Human secreted protein encoded by 5' EST clone 58-34-2-E7-FL2.
PN WO9906552-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.
Query Match 25.3%; Score 352; DB 2; Length 69;
Best Local Similarity 98.5%; Pred. No. 1e-31;
RESULT 710
ID AAY25451 standard; protein; 69 AA.
DE Human secreted protein 2 derived from extended cDNA.
PN WO9925825-A2.
PD 27-MAY-1999.
PA (GEST) GENSET.
Query Match 25.3%; Score 352; DB 2; Length 69;
Best Local Similarity 98.5%; Pred. No. 1e-31;
RESULT 711
ID AAY12672 standard; peptide; 69 AA.
DE Human 5' EST secreted protein.
PN WO9906549-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.
Query Match 25.3%; Score 352; DB 2; Length 69;
Best Local Similarity 98.5%; Pred. No. 1e-31;
RESULT 712
ID AAY12672 standard; peptide; 69 AA.
DE Human 5' EST secreted protein.
PN WO9906549-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.
Query Match 25.3%; Score 352; DB 2; Length 69;
Best Local Similarity 98.5%; Pred. No. 1e-31;

ID AAG00010 standard; protein; 69 AA.
DE Human secreted protein #1.
PN EP103401-A2.
PD 06-SEP-2000.
PA (GEST) GENSET.
Query Match 25.3%; Score 352; DB 3; Length 69;
Best Local Similarity 98.5%; Pred. No. 1e-31;
RESULT 713
ID ADU73027 standard; protein; 69 AA.
DE cDNA 58-34-2-E7-FL2-encoded secreted protein, SEQ ID NO:1.
PN US6822072-B1.
PD 23-NOV-2004.
PA (GEST) GENSET SA.
Query Match 25.3%; Score 352; DB 8; Length 69;
Best Local Similarity 98.5%; Pred. No. 1e-31;
RESULT 714
ID ABB89768 standard; protein; 180 AA.
DE Human polypeptide SEQ ID NO 2144.
PN WO200190304-A2.
PD 29-NOV-2001.
PA (HUNA-) HUMAN GENOME SCI INC.
Query Match 22.8%; Score 317.5; DB 5; Length 180;
Best Local Similarity 33.3%; Pred. No. 3.2e-27;
RESULT 715
ID AAG81279 standard; protein; 114 AA.
DE Human APP protein sequence SEQ ID NO:76.
PN WO200129221-A2.
PD 26-APR-2001.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 19.6%; Score 272.5; DB 4; Length 114;
Best Local Similarity 47.5%; Pred. No. 2.2e-22;
RESULT 716
ID AAB93632 standard; protein; 132 AA.
DE Human protein sequence SEQ ID NO:13115.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 18.0%; Score 251; DB 4; Length 132;
Best Local Similarity 33.3%; Pred. No. 7.4e-20;
RESULT 717
ID ADL06520 standard; protein; 132 AA.
DE Human tumour-associated antigenic target (TAT) polypeptide #19.
PN WO2004016225-A2.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 18.0%; Score 251; DB 8; Length 132;
Best Local Similarity 33.3%; Pred. No. 7.4e-20;
RESULT 718
ID ADJ75472 standard; protein; 132 AA.
DE Marker gene related amino acid sequence SEQ ID NO:724.
PN EP1394274-A2.
PD 03-MAR-2004.
PA (GENO-) GENOX RES INC.
Query Match 18.0%; Score 251; DB 8; Length 132;
Best Local Similarity 33.3%; Pred. No. 7.4e-20;
RESULT 719
ID ADRI4452 standard; protein; 132 AA.
DE Human NF-kappaB pathway-associated protein SeqID453.
PN WO2004065577-A2.
PD 05-AUG-2004.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 18.0%; Score 251; DB 8; Length 132;
Best Local Similarity 33.3%; Pred. No. 7.4e-20;
RESULT 720
ID ADP24981 standard; protein; 132 AA.
DE PRO polypeptide SEQ ID NO:2159.
PN WO2004041170-A2.
PD 21-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 18.0%; Score 251; DB 8; Length 132;
Best Local Similarity 33.3%; Pred. No. 7.4e-20;
RESULT 721
ID ADU06610 standard; protein; 132 AA.

DE Novel bronchial cancer-associated human protein SeqID836.
PN DE10316701-A1.
PD 04-NOV-2004.
PA (HINZ/) HINZMANN B.
PA (HERM/) HERMANN K.
PA (CAST/) HEIDEN CASTANOS-VELEZ E.
Query Match 18.0%; Score 251; DB 8; Length 132;
Best Local Similarity 33.3%; Pred. No. 7.4e-20;
RESULT 722
ID ADS11008 standard; protein; 233 AA.
DE Human therapeutic protein - SEQ ID 1245.
PN WO2004080148-A2.
PD 23-SEP-2004.
PA (NUVE-) NUVELO INC.
Query Match 15.8%; Score 220.5; DB 8; Length 233;
Best Local Similarity 27.2%; Pred. No. 4.7e-16;
RESULT 723
ID ABO00507 standard; protein; 283 AA.
DE Novel human polypeptide #94.
PN WO2003023013-A2.
PD 20-MAR-2003.
PA (HYSE-) HYSEQ INC.
Query Match 15.4%; Score 214.5; DB 6; Length 283;
Best Local Similarity 26.2%; Pred. No. 3e-15;
RESULT 724
ID AAB08866 standard; protein; 249 AA.
DE Amino acid sequence of a human secretory protein.
PN WO200052151-A2.
PD 08-SEP-2000.
PA (INCY-) INCYTE PHARM INC.
Query Match 15.2%; Score 212; DB 3; Length 249;
Best Local Similarity 26.5%; Pred. No. 4.8e-15;
RESULT 725
ID AM38964 standard; protein; 249 AA.
DE Human polypeptide SEQ ID NO 2109.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 15.2%; Score 212; DB 4; Length 249;
Best Local Similarity 26.5%; Pred. No. 4.8e-15;
RESULT 726
ID AAM51628 standard; protein; 249 AA.
DE Human plasminogen activator inhibitor 2-27 polypeptide.
PN CN1313331-A.
PD 19-SEP-2001.
PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
Query Match 15.2%; Score 212; DB 5; Length 249;
Best Local Similarity 26.5%; Pred. No. 4.8e-15;
RESULT 727
ID ADP18677 standard; protein; 249 AA.
DE Human protein encoded by TAT414 cDNA used to treat cancer SeqID 37.
PN WO2004045516-A2.
PD 03-JUN-2004.
PA (GETH) GENENTECH INC.
Query Match 15.2%; Score 212; DB 8; Length 249;
Best Local Similarity 26.5%; Pred. No. 4.8e-15;
RESULT 728
ID AAV12179 standard; protein; 36 AA.
DE Human 5' EST secreted protein SEQ ID NO: 492.
PN WO9906554-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.
Query Match 14.0%; Score 195; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 2.9e-14;
RESULT 729
ID AAM40750 standard; protein; 274 AA.
DE Human polypeptide SEQ ID NO 5681.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 13.8%; Score 192.5; DB 4; Length 274;
Best Local Similarity 31.4%; Pred. No. 9e-13;
RESULT 730

ID ABG17213 standard; protein; 308 AA.
DE Novel human diagnostic protein #17204.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 12.9%; Score 180; DB 4; Length 308;
Best Local Similarity 100.0%; Pred. No. 2.8e-11;
RESULT 731
ID ABG16460 standard; protein; 466 AA.
DE Novel human diagnostic protein #16451.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 12.7%; Score 176.5; DB 4; Length 466;
Best Local Similarity 60.0%; Pred. No. 1.2e-10;
RESULT 732
ID AAE00332 standard; protein; 253 AA.
DE Human membrane-bound protein-60 alternative mature protein sequence.
PN WO200123567-A1.
PD 05-APR-2001.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 11.5%; Score 160.5; DB 4; Length 253;
Best Local Similarity 24.5%; Pred. No. 3.5e-09;
RESULT 733
ID AAE00331 standard; protein; 256 AA.
DE Human membrane-bound protein-60 (Zsig60) mature protein sequence.
PN WO200123567-A1.
PD 05-APR-2001.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 11.5%; Score 160.5; DB 4; Length 256;
Best Local Similarity 24.5%; Pred. No. 3.5e-09;
RESULT 734
ID AAB18985 standard; protein; 271 AA.
DE Amino acid sequence of a human transmembrane protein.
PN WO200056891-A2.
PD 28-SEP-2000.
PA (INCY-) INCYTE PHARM INC.
Query Match 11.5%; Score 160.5; DB 3; Length 271;
Best Local Similarity 24.5%; Pred. No. 3.8e-09;
RESULT 735
ID AAE00330 standard; protein; 271 AA.
DE Human membrane-bound protein-60 (Zsig60).
PN WO200123567-A1.
PD 05-APR-2001.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 11.5%; Score 160.5; DB 4; Length 271;
Best Local Similarity 24.5%; Pred. No. 3.8e-09;
RESULT 736
ID AAY48244 standard; protein; 304 AA.
DE Human prostate cancer-associated protein 30.
PN DE19811193-A1.
PD 16-SEP-1999.
PA (META-) METAGEN GBS GENOMFORSCHUNG MBH.
Query Match 10.9%; Score 152; DB 2; Length 304;
Best Local Similarity 24.0%; Pred. No. 4.1e-08;
RESULT 737
ID AAE00334 standard; protein; 160 AA.
DE Human membrane-bound protein-60 alternative mature extracellular portion.
PN WO200123567-A1.
PD 05-APR-2001.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 10.9%; Score 151.5; DB 4; Length 160;
Best Local Similarity 29.5%; Pred. No. 1.9e-08;
RESULT 738
ID AAE00333 standard; protein; 163 AA.
DE Human membrane-bound protein-60 (Zsig60) mature extracellular portion.
PN WO200123567-A1.
PD 05-APR-2001.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 10.9%; Score 151.5; DB 4; Length 163;
Best Local Similarity 29.5%; Pred. No. 2e-08;
RESULT 739
ID AAY94930 standard; protein; 437 AA.

DE Human secreted protein clone qal36_1 protein sequence SEQ ID NO:66.
PN WO200009552-A1.
PD 24-FEB-2000.
PA (GEMY) GENETICS INST INC.
Query Match 10.9%; Score 151.5; DB 3; Length 437;
Best Local Similarity 26.8%; Pred. No. 7.7e-08;
RESULT 740
ID AAY95013 standard; protein; 178 AA.
DE Human secreted protein vc48_1, SEQ ID NO:66.
PN WO200011015-A1.
PD 02-MAR-2000.
PA (ALPH-) ALPHAGENE INC.
Query Match 10.6%; Score 147.5; DB 3; Length 178;
Best Local Similarity 24.9%; Pred. No. 6.4e-08;
RESULT 741
ID ADN02727 standard; protein; 255 AA.
DE Human receptor and membrane -associated protein #30.
PN WO2004029218-A2.
PD 08-APR-2004.
PA (INCY-) INCYTE CORP.
Query Match 10.5%; Score 146.5; DB 8; Length 255;
Best Local Similarity 24.6%; Pred. No. 1.4e-07;
RESULT 742
ID ABO00615 standard; protein; 63 AA.
DE Novel human polypeptide #202.
PN WO2003023013-A2.
PD 20-MAR-2003.
PA (HYSE-) HYSEQ INC.
Query Match 9.1%; Score 126; DB 6; Length 63;
Best Local Similarity 47.2%; Pred. No. 4.2e-06;
RESULT 743
ID ADS11007 standard; protein; 127 AA.
DE Human therapeutic protein - SEQ ID 1244.
PN WO2004080148-A2.
PD 23-SEP-2004.
PA (NUVE-) NUVELO INC.
Query Match 8.8%; Score 122.5; DB 8; Length 127;
Best Local Similarity 32.1%; Pred. No. 2.8e-05;
RESULT 744
ID AAY04149 standard; peptide; 21 AA.
DE Human secreted protein 5' EST signal peptide SEQ ID NO:20.
PN WO9906439-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.
Query Match 8.5%; Score 118; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 7.6e-06;
RESULT 745
ID AAY11369 standard; protein; 21 AA.
DE Human 5' EST secreted protein SEQ ID NO:20.
PN WO9906551-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.
Query Match 8.5%; Score 118; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 7.6e-06;
RESULT 746
ID AAY12516 standard; peptide; 21 AA.
DE Human 5' EST signal peptide SEQ ID NO: 20 from WO 9906553.
PN WO9906553-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.
Query Match 8.5%; Score 118; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 7.6e-06;
RESULT 747
ID AAY35883 standard; peptide; 21 AA.
DE Signal peptide of extended secreted protein, SEQ ID NO. 20.
PN WO991236-A2.
PD 24-JUN-1999.
PA (GEST) GENSET.
Query Match 8.5%; Score 118; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 7.6e-06;
RESULT 748
ID AAY59644 standard; peptide; 21 AA.
DE Secreted protein extended EST signal peptide #2.

Best Local Similarity 22.8%; Pred. No. 0.016;
RESULT 766
ID AEB38816 standard; protein; 581 AA.
DE L. pneumophila protein SEQ ID NO 3148.
PN WO2005049642-A2.
PD 02-JUN-2005.
PA (INSP) INST PASTEUR.
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
PA (UYLY-) UNIV LYON 1 BERNARD CLAUDE.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 7.1%; Score 99.5; DB 9; Length 581;
Best Local Similarity 24.4%; Pred. No. 0.092;
RESULT 767
ID ADM06102 standard; protein; 187 AA.
DE Human protein of the invention SEQ ID NO:4787.
PN EP1347046-A1.
PD 24-SEP-2003.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 7.1%; Score 99; DB 7; Length 187;
Best Local Similarity 23.4%; Pred. No. 0.022;
RESULT 768
ID AEC89032 standard; protein; 187 AA.
DE Human cDNA clone protein TRACH20128110, SEQ ID 4787.
PN EP1580263-A1.
PD 28-SEP-2005.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 7.1%; Score 99; DB 9; Length 187;
Best Local Similarity 23.4%; Pred. No. 0.022;
RESULT 769
ID ABU45347 standard; protein; 1066 AA.
DE Protein encoded by Prokaryotic essential gene #30874.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 7.1%; Score 98.5; DB 6; Length 1066;
Best Local Similarity 19.5%; Pred. No. 0.28;
RESULT 770
ID ABU47563 standard; protein; 1120 AA.
DE Protein encoded by Prokaryotic essential gene #33090.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 7.1%; Score 98.5; DB 6; Length 1120;
Best Local Similarity 19.5%; Pred. No. 0.3;
RESULT 771
ID ABU46980 standard; protein; 1120 AA.
DE Protein encoded by Prokaryotic essential gene #32507.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 7.1%; Score 98.5; DB 6; Length 1120;
Best Local Similarity 19.5%; Pred. No. 0.3;
RESULT 772
ID AEB42187 standard; protein; 268 AA.
DE L. pneumophila protein SEQ ID NO 6519.
PN WO2005049642-A2.
PD 02-JUN-2005.
PA (INSP) INST PASTEUR.
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
PA (UYLY-) UNIV LYON 1 BERNARD CLAUDE.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 6.8%; Score 94.5; DB 9; Length 268;
Best Local Similarity 22.8%; Pred. No. 0.12;
RESULT 773
ID AEB39048 standard; protein; 291 AA.
DE L. pneumophila protein SEQ ID NO 3380.
PN WO2005049642-A2.
PD 02-JUN-2005.
PA (INSP) INST PASTEUR.
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
PA (UYLY-) UNIV LYON 1 BERNARD CLAUDE.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 6.8%; Score 94.5; DB 9; Length 291;

Best Local Similarity 22.6%; Pred. No. 0.13;
RESULT 774
ID ABU34113 standard; protein; 548 AA.
DE Protein encoded by Prokaryotic essential gene #19640.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.8%; Score 94.5; DB 6; Length 548;
Best Local Similarity 18.2%; Pred. No. 0.31;
RESULT 775
ID ABU39811 standard; protein; 269 AA.
DE Protein encoded by Prokaryotic essential gene #25338.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.8%; Score 94; DB 6; Length 269;
Best Local Similarity 21.7%; Pred. No. 0.13;
RESULT 776
ID AEC57250 standard; protein; 452 AA.
DE L. acidophilus maltose ABC transporter permease SEQ ID 64.
PN WO2005084411-A2.
PD 15-SEP-2005.
PA (UYNC-) UNIV NORTH CAROLINA STATE.
Query Match 6.8%; Score 94; DB 9; Length 452;
Best Local Similarity 19.2%; Pred. No. 0.27;
RESULT 777
ID AAG44537 standard; protein; 303 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 55801.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.7%; Score 93.5; DB 3; Length 303;
Best Local Similarity 21.8%; Pred. No. 0.18;
RESULT 778
ID AAG44536 standard; protein; 367 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 55800.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.7%; Score 93.5; DB 3; Length 367;
Best Local Similarity 21.8%; Pred. No. 0.24;
RESULT 779
ID ABU15091 standard; protein; 1120 AA.
DE Protein encoded by Prokaryotic essential gene #618.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.7%; Score 93; DB 6; Length 1120;
Best Local Similarity 19.6%; Pred. No. 1.2;
RESULT 780
ID ABU47616 standard; protein; 473 AA.
DE Protein encoded by Prokaryotic essential gene #33143.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.6%; Score 92.5; DB 6; Length 473;
Best Local Similarity 22.8%; Pred. No. 0.43;
RESULT 781
ID ABB89477 standard; protein; 118 AA.
DE Human polypeptide SEQ ID NO 1853.
PN WO200190304-A2.
PD 29-NOV-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.6%; Score 91.5; DB 5; Length 118;
Best Local Similarity 28.0%; Pred. No. 0.083;
RESULT 782
ID ADC94520 standard; protein; 291 AA.
DE E. faecium protein sequence SEQ ID 4147.
PN US6583275-B1.
PD 24-JUN-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 6.6%; Score 91.5; DB 7; Length 291;
Best Local Similarity 22.9%; Pred. No. 0.29;
RESULT 783
ID ADN23444 standard; protein; 373 AA.

DE Bacterial polypeptide #6097.
PN US2003233675-A1.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 6.6%; Score 91.5; DB 8; Length 373;
Best Local Similarity 23.0%; Pred. No. 0.41;
RESULT 784
ID AAU03808 standard; protein; 387 AA.
DE G protein-coupled receptor-like (GPCR-like) receptor protein #7.
PN WO200138533-A2.
PD 31-MAY-2001.
PA (PHAA) PHARMACIA & UPJOHN.
Query Match 6.6%; Score 91.5; DB 4; Length 387;
Best Local Similarity 23.0%; Pred. No. 0.43;
RESULT 785
ID ABB91939 standard; protein; 712 AA.
DE Herbicidally active polypeptide SEQ ID NO 1150.
PN WO200210210-A2.
PD 07-FEB-2002.
PA (FARB) BAYER AG.
Query Match 6.6%; Score 91.5; DB 5; Length 712;
Best Local Similarity 22.2%; Pred. No. 0.99;
RESULT 786
ID ADX68404 standard; protein; 486 AA.
DE Plant full length insert polypeptide seqid 39247.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 6.5%; Score 91; DB 8; Length 486;
Best Local Similarity 22.6%; Pred. No. 0.67;
RESULT 787
ID ADX87645 standard; protein; 486 AA.
DE Plant full length insert polypeptide seqid 50309.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 6.5%; Score 91; DB 8; Length 486;
Best Local Similarity 22.6%; Pred. No. 0.67;
RESULT 788
ID ADY12322 standard; protein; 487 AA.
DE Plant full length insert polypeptide seqid 68137.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 6.5%; Score 91; DB 8; Length 487;
Best Local Similarity 22.6%; Pred. No. 0.67;
RESULT 789
ID ADN46339 standard; protein; 451 AA.
DE Thermococcus kodakaraensis KOD1 protein sequence SeqID217.
PN WO2004022736-A1.
PD 18-MAR-2004.
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
Query Match 6.5%; Score 90.5; DB 8; Length 451;
Best Local Similarity 21.2%; Pred. No. 0.68;

RESULT 790
ID AAB76803 standard; protein; 283 AA.
DE Corynebacterium glutamicum MCT protein SEQ ID NO:588.
PN WO200100805-A2.
PD 04-JAN-2001.
PA (BADI) BASF AG.
Query Match 6.5%; Score 90; DB 4; Length 283;
Best Local Similarity 23.8%; Pred. No. 0.41;
RESULT 791
ID AAG89779 standard; protein; 283 AA.
DE C glutamicum protein fragment SEQ ID NO: 3533.
PN EPI108790-A2.
PD 20-JUN-2001.
PA (KYOW) KYOWA HAKKO KOGYO KK.
Query Match 6.5%; Score 90; DB 4; Length 283;
Best Local Similarity 23.8%; Pred. No. 0.41;
RESULT 792
ID AED46975 standard; protein; 283 AA.
DE Membrane construction and membrane transport protein SEQ ID 252.
PN US200524935-A1.
PD 03-NOV-2005.
PA (BADI) BASF AG.
Query Match 6.5%; Score 90; DB 9; Length 283;
Best Local Similarity 23.8%; Pred. No. 0.41;
RESULT 793
ID AED46977 standard; protein; 283 AA.
DE Membrane construction and membrane transport protein SEQ ID 254.
PN US200524935-A1.
PD 03-NOV-2005.
PA (BADI) BASF AG.
Query Match 6.5%; Score 90; DB 9; Length 283;
Best Local Similarity 23.8%; Pred. No. 0.41;
RESULT 794
ID ADP98865 standard; protein; 505 AA.
DE C. albicans specific gene, orif6.4442, protein sequence.
PN WO2004056365-A2.
PD 08-JUL-2004.
PA (ELIT-) ELITRA PHARM INC.
PA (ELIT-) ELITRA CANADA LTD.
Query Match 6.5%; Score 90; DB 8; Length 505;
Best Local Similarity 20.5%; Pred. No. 0.91;
RESULT 795
ID ABU45537 standard; protein; 458 AA.
DE Protein encoded by Prokaryotic essential gene #31064.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.4%; Score 89.5; DB 6; Length 458;
Best Local Similarity 22.8%; Pred. No. 0.91;
RESULT 796
ID ABP26393 standard; protein; 579 AA.
DE Streptococcus polypeptide SEQ ID NO 1962.
PN WO200234771-A2.
PD 02-MAY-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match 6.4%; Score 89.5; DB 5; Length 579;
Best Local Similarity 24.8%; Pred. No. 1.3;
RESULT 797
ID ADV88815 standard; protein; 579 AA.
DE Streptococcus agalactiae protein sequence, SEQ ID 1209.
PN FR2824074-A1.
PD 31-OCT-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 6.4%; Score 89.5; DB 8; Length 579;
Best Local Similarity 24.8%; Pred. No. 1.3;
RESULT 798
ID ADV82204 standard; protein; 579 AA.
DE Streptococcus agalactiae protein, SEQ ID 3345.
PN WO200292818-A2.
PD 21-NOV-2002.
PA (INSP) INST PASTEUR.

PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 6.4%; Score 89.5; DB 8; Length 579;
Best Local Similarity 24.8%; Pred. No. 1.3;
RESULT 799
ID ADV80068 standard; protein; 579 AA.
DE Streptococcus agalactiae protein, SEQ ID 1209.
PN WO2002922818-A2.
PD 21-NOV-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 6.4%; Score 89.5; DB 8; Length 579;
Best Local Similarity 24.8%; Pred. No. 1.3;
RESULT 800
ID ABU50406 standard; protein; 428 AA.
DE Protein encoded by Prokaryotic essential gene #35933.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.4%; Score 89; DB 6; Length 428;
Best Local Similarity 21.6%; Pred. No. 0.94;
RESULT 801
ID AAB94689 standard; protein; 637 AA.
DE Human protein sequence SEQ ID NO:15654.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 6.4%; Score 89; DB 4; Length 637;
Best Local Similarity 21.5%; Pred. No. 1.6;
RESULT 802
ID ABU23408 standard; protein; 642 AA.
DE Protein encoded by Prokaryotic essential gene #8935.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.4%; Score 89; DB 6; Length 642;
Best Local Similarity 20.8%; Pred. No. 1.6;
RESULT 803
ID RAU03497 standard; protein; 757 AA.
DE Human sterol sensing domain protein.
PN WO200146227-A2.
PD 28-JUN-2001.
PA (UYZU-) UNIV ZURICH.
Query Match 6.4%; Score 89; DB 4; Length 757;
Best Local Similarity 21.5%; Pred. No. 2.1;
RESULT 804
ID AAB41293 standard; protein; 758 AA.
DE Human ORFX ORF1057 polypeptide sequence SEQ ID NO:2114.
PN WO200058473-A2.
PD 05-OCT-2000.
PA (CURA-) CURAGEN CORP.
Query Match 6.4%; Score 89; DB 3; Length 758;
Best Local Similarity 21.5%; Pred. No. 2.1;
RESULT 805
ID AAU74820 standard; protein; 1124 AA.
DE Human RPT3 protein.
PN WO200198354-A2.
PD 27-DEC-2001.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 6.4%; Score 89; DB 5; Length 1124;
Best Local Similarity 21.5%; Pred. No. 3.6;
RESULT 806
ID ADA55083 standard; protein; 1203 AA.
DE Human protein, SEQ ID 2651.
PN EP1293569-A2.
PD 19-MAR-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 6.4%; Score 89; DB 6; Length 1203;
Best Local Similarity 21.5%; Pred. No. 3.9;
RESULT 807
ID ABG31547 standard; protein; 1330 AA.
DE Human patched-like protein.
PN WO200246402-A2.

PD 13-JUN-2002.
PA (FARB) BAYER AG.
Query Match 6.4%; Score 89; DB 5; Length 1330;
Best Local Similarity 21.5%; Pred. No. 4.5;
RESULT 808
ID AEB40780 standard; protein; 361 AA.
DE L. pneumophila protein SEQ ID NO 5112.
PN WO2005049642-A2.
PD 02-JUN-2005.
PA (INSP) INST PASTEUR.
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
PA (UYLY-) UNIV LYON 1 BERNARD CLAUDE.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 6.4%; Score 88.5; DB 9; Length 361;
Best Local Similarity 20.9%; Pred. No. 0.85;
RESULT 809
ID ADY10982 standard; protein; 372 AA.
DE Plant full length insert polypeptide seqid 66797.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 6.4%; Score 88.5; DB 8; Length 372;
Best Local Similarity 19.3%; Pred. No. 0.89;
RESULT 810
ID AEB37466 standard; protein; 374 AA.
DE L. pneumophila protein SEQ ID NO 1798.
PN WO2005049642-A2.
PD 02-JUN-2005.
PA (INSP) INST PASTEUR.
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
PA (UYLY-) UNIV LYON 1 BERNARD CLAUDE.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 6.4%; Score 88.5; DB 9; Length 374;
Best Local Similarity 20.9%; Pred. No. 0.89;
RESULT 811
ID AAB96747 standard; protein; 430 AA.
DE Putative P. abyss permease #26.
PN FR2792651-A1.
PD 27-OCT-2000.
PA (CNRS) CNRS CENT NAT RECH SCI.
PA (IFRE-) IFREMER INST FR RECH EXPL MER.
Query Match 6.4%; Score 88.5; DB 4; Length 430;
Best Local Similarity 23.8%; Pred. No. 1.1;
RESULT 812
ID AAR37309 standard; protein; 1165 AA.
DE Cardiac adenyllyl cyclase.
PN EP543137-A1.
PD 26-MAY-1993.
PA (AMCY) AMERICAN CYANAMID CO.
Query Match 6.3%; Score 88; DB 2; Length 1165;
Best Local Similarity 20.5%; Pred. No. 4.9;
RESULT 813
ID ABU19097 standard; protein; 233 AA.
DE Protein encoded by Prokaryotic essential gene #4624.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.3%; Score 87.5; DB 6; Length 233;
Best Local Similarity 22.8%; Pred. No. 0.6;
RESULT 814
ID ADD67113 standard; protein; 322 AA.
DE Homogentisate prenyl transferase.
PN WO2003080647-A2.
PD 02-OCT-2003.
PA (MONS) MONSANTO TECHNOLOGY LLC.
Query Match 6.3%; Score 87.5; DB 7; Length 322;
Best Local Similarity 22.6%; Pred. No. 0.94;
RESULT 815

ID ADC77581 standard; protein; 453 AA.
DE Mouse TMS2 amino acid sequence.
PN WO2003066829-A2.
PD 14-AUG-2003.
PA (DISC-) DISCOVERY GENOMICS INC.
Query Match 6.3%; Score 87.5; DB 7; Length 453;
Best Local Similarity 19.9%; Pred. No. 1.5;
RESULT 816
ID ADS28619 standard; protein; 482 AA.
DE Bacterial polypeptide #17652.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 6.3%; Score 87.5; DB 8; Length 482;
Best Local Similarity 21.2%; Pred. No. 1.6;
RESULT 817
ID AEB38041 standard; protein; 521 AA.
DE L. pneumophila protein SEQ ID NO 2373.
PN WO2005049642-A2.
PD 02-JUN-2005.
PA (INSP) INST PASTEUR.
PA (INRM) INERM INST NAT SANTE & RECH MEDICALE.
PA (UYLY-) UNIV LYON 1 BERNARD CLAUDE.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 6.3%; Score 87.5; DB 9; Length 521;
Best Local Similarity 22.5%; Pred. No. 1.8;
RESULT 818
ID AEB41335 standard; protein; 521 AA.
DE L. pneumophila protein SEQ ID NO 5667.
PN WO2005049642-A2.
PD 02-JUN-2005.
PA (INSP) INST PASTEUR.
PA (INRM) INERM INST NAT SANTE & RECH MEDICALE.
PA (UYLY-) UNIV LYON 1 BERNARD CLAUDE.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 6.3%; Score 87.5; DB 9; Length 521;
Best Local Similarity 22.5%; Pred. No. 1.8;
RESULT 819
ID AEB41995 standard; protein; 535 AA.
DE L. pneumophila protein SEQ ID NO 6327.
PN WO2005049642-A2.
PD 02-JUN-2005.
PA (INSP) INST PASTEUR.
PA (INRM) INERM INST NAT SANTE & RECH MEDICALE.
PA (UYLY-) UNIV LYON 1 BERNARD CLAUDE.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 6.2%; Score 87; DB 9; Length 535;
Best Local Similarity 26.0%; Pred. No. 2.2;
RESULT 820
ID ABU33543 standard; protein; 239 AA.
DE Protein encoded by Prokaryotic essential gene #19070.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.2%; Score 86.5; DB 6; Length 239;
Best Local Similarity 20.4%; Pred. No. 0.81;
RESULT 821
ID ADT05661 standard; protein; 261 AA.
DE Haemophilus influenzae (NTH) protein - SEQ ID 697.
PN WO2004078949-A2.
PD 16-SEP-2004.
PA (CHIL-) CHILDRENS HOSPITAL INC.
Query Match 6.2%; Score 86.5; DB 8; Length 261;
Best Local Similarity 24.2%; Pred. No. 0.92;
RESULT 822
ID ADH87029 standard; protein; 356 AA.
DE Enterococcus faecalis polypeptide #1509.
PN US6617156-B1.
PD 09-SEP-2003.
PA (DOUC/) DOUCETTE-STAMM L A.
PA (BUSH/) BUSH D.
Query Match 6.2%; Score 86.5; DB 7; Length 356;
Best Local Similarity 19.2%; Pred. No. 1.4;
RESULT 823
ID ADS44642 standard; protein; 400 AA.
DE Bacterial polypeptide #23072.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 6.2%; Score 86.5; DB 8; Length 400;
Best Local Similarity 21.9%; Pred. No. 1.7;
RESULT 824
ID ABB47717 standard; protein; 583 AA.
DE Listeria monocytogenes protein #421.
PN WO200177335-A2.
PD 18-OCT-2001.
PA (INSP) INST PASTEUR.
Query Match 6.2%; Score 86.5; DB 5; Length 583;
Best Local Similarity 19.4%; Pred. No. 2.8;
RESULT 825
ID AAG39112 standard; protein; 1346 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 48347.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.2%; Score 86.5; DB 3; Length 1346;
Best Local Similarity 18.2%; Pred. No. 8.8;
RESULT 826
ID AAG39111 standard; protein; 1390 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 48346.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.2%; Score 86.5; DB 3; Length 1390;
Best Local Similarity 18.2%; Pred. No. 9.2;
RESULT 827
ID AAG39110 standard; protein; 1403 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 48345.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.2%; Score 86.5; DB 3; Length 1403;
Best Local Similarity 18.2%; Pred. No. 9.3;
RESULT 828
ID ABM73219 standard; protein; 372 AA.
DE Staphylococcus aureus protein #2459.
PN WO200294868-A2.
PD 28-NOV-2002.
PA (CHIR-) CHIRON SPA.
Query Match 6.2%; Score 86; DB 6; Length 372;
Best Local Similarity 18.1%; Pred. No. 1.7;
RESULT 829
ID AAG98347 standard; protein; 396 AA.
DE Escherichia coli protein sequence SEQ ID NO:395.
PN WO200148209-A2.
PD 05-JUL-2001.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.2%; Score 86; DB 4; Length 396;
Best Local Similarity 21.9%; Pred. No. 1.9;
RESULT 830
ID ABU14798 standard; protein; 396 AA.
DE Protein encoded by Prokaryotic essential gene #325.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.2%; Score 86; DB 6; Length 396;
Best Local Similarity 21.9%; Pred. No. 1.9;
RESULT 831
ID ABB90798 standard; protein; 725 AA.
DE Herbicidally active polypeptide SEQ ID NO 9.
PN WO200210210-A2.

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PD 07-FEB-2002.
PA (FARB) BAYER AG.
Query Match 6.1%; Score 86; DB 5; Length 725;
Best Local Similarity 18.9%; Pred. No. 4.3;
RESULT 832
ID AAB11039 standard; protein; 841 AA.
DE S. xylopus mprF protein.
PN DE19914817-A1.
PD 05-OCT-2000.
PA (PETR-) PETRY GENMEDICS GMBH.
Query Match 6.2%; Score 86; DB 3; Length 841;
Best Local Similarity 18.3%; Pred. No. 5.2;
RESULT 833
ID ABP77912 standard; protein; 295 AA.
DE N. gonorrhoeae amino acid sequence SEQ ID 2354.
PN WO200279243-A2.
PD 10-OCT-2002.
PA (CHIR-) CHIRON SPA.
Query Match 6.1%; Score 85.5; DB 6; Length 295;
Best Local Similarity 21.6%; Pred. No. 1.4;
RESULT 834
ID ABU37235 standard; protein; 295 AA.
DE Protein encoded by Prokaryotic essential gene #22762.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.1%; Score 85.5; DB 6; Length 295;
Best Local Similarity 21.6%; Pred. No. 1.4;
RESULT 835
ID ABJ39122 standard; protein; 311 AA.
DE Molecule for disease detection and treatment (MDDT)-32 protein sequence.
PN WO2003052049-A2.
PD 26-JUN-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 6.1%; Score 85.5; DB 6; Length 311;
Best Local Similarity 21.7%; Pred. No. 1.5;
RESULT 836
ID ADC37363 standard; protein; 311 AA.
DE Nuclear factor kappa B (NF-kappaB) activating protein, SEQ ID 196.
PN WO2003048202-A2.
PD 12-JUN-2003.
PA (ASAH) ASAH KASEI KK.
Query Match 6.1%; Score 85.5; DB 7; Length 311;
Best Local Similarity 21.7%; Pred. No. 1.5;
RESULT 837
ID ADR58959 standard; protein; 311 AA.
DE Human E1k1 phosphorylation/E1k1 kinase activation protein - SEQ ID 62.
PN WO2004072277-A2.
PD 26-AUG-2004.
PA (ASAH-) ASAH KASEI PHARMA CORP.
Query Match 6.1%; Score 85.5; DB 8; Length 311;
Best Local Similarity 21.7%; Pred. No. 1.5;
RESULT 838
ID ADU76431 standard; protein; 311 AA.
DE Progesterone-YOL002C-CGI-45 receptor, INTP047.
PN WO2004101618-A2.
PD 25-NOV-2004.
PA (INPH-) INPHARMATICA LTD.
Query Match 6.1%; Score 85.5; DB 8; Length 311;
Best Local Similarity 21.7%; Pred. No. 1.5;
RESULT 839
ID AAM93524 standard; protein; 329 AA.
DE Human polypeptide, SEQ ID NO: 3257.
PN EP130094-A2.
PD 05-SEP-2001.
PA (HELI-) HELIX RES INST.
Query Match 6.1%; Score 85.5; DB 4; Length 329;
Best Local Similarity 23.0%; Pred. No. 1.6;
RESULT 840
ID AAB92687 standard; protein; 329 AA.
DE Human protein sequence SEQ ID NO:11071.
PN EP1074617-A2.
PD 07-FEB-2001.

PA (HELI-) HELIX RES INST.
Query Match 6.1%; Score 85.5; DB 4; Length 329;
Best Local Similarity 23.0%; Pred. No. 1.6;
RESULT 841
ID ADL31224 standard; protein; 329 AA.
DE Human protein encoded by a full length cDNA clone SeqID 3257.
PN EP1396543-A2.
PD 10-MAR-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 6.1%; Score 85.5; DB 8; Length 329;
Best Local Similarity 23.0%; Pred. No. 1.6;
RESULT 842
ID ADA98171 standard; protein; 359 AA.
DE Human secreted protein sequence #12.
PN WO2003004623-A2.
PD 16-JAN-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.1%; Score 85.5; DB 6; Length 359;
Best Local Similarity 23.0%; Pred. No. 1.8;
RESULT 843
ID ADA44024 standard; protein; 359 AA.
DE Human secreted protein SEQ ID 212.
PN WO2003000865-A2.
PD 03-JAN-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.1%; Score 85.5; DB 6; Length 359;
Best Local Similarity 23.0%; Pred. No. 1.8;
RESULT 844
ID ADC20341 standard; protein; 359 AA.
DE Human secreted protein - amino acid sequence #17.
PN WO200292787-A2.
PD 21-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.1%; Score 85.5; DB 7; Length 359;
Best Local Similarity 23.0%; Pred. No. 1.8;
RESULT 845
ID ADF10683 standard; protein; 359 AA.
DE Human secreted protein #5.
PN WO200299085-A2.
PD 12-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.1%; Score 85.5; DB 7; Length 359;
Best Local Similarity 23.0%; Pred. No. 1.8;
RESULT 846
ID AAB75546 standard; protein; 360 AA.
DE Human secreted protein sequence encoded by gene 41 SEQ ID NO:100.
PN WO200077036-A1.
PD 21-DEC-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.1%; Score 85.5; DB 4; Length 360;
Best Local Similarity 23.0%; Pred. No. 1.9;
RESULT 847
ID AAM61371 standard; protein; 439 AA.
DE Non-adrenergic SM binding protein.
PN EP848059-A1.
PD 17-JUN-1998.
PA (VETI-) VETIGEN.
Query Match 6.1%; Score 85.5; DB 2; Length 439;
Best Local Similarity 23.0%; Pred. No. 2.4;
RESULT 848
ID AAB75598 standard; protein; 530 AA.
DE Human secreted protein sequence encoded by gene 41 SEQ ID NO:152.
PN WO200077026-A1.
PD 21-DEC-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.1%; Score 85.5; DB 4; Length 530;
Best Local Similarity 23.0%; Pred. No. 3.2;
RESULT 849
ID AAY94910 standard; protein; 545 AA.
DE Human secreted protein clone pk366_7 protein sequence SEQ ID NO:26.
PN WO200009552-A1.

PD 24-FEB-2000.
PA (GENY) GENETICS INST INC.
Query Match 6.1%; Score 85.5; DB 3; Length 545;
Best Local Similarity 23.0%; Pred. No. 3.3;
RESULT 850
ID AAB94667 standard; protein; 545 AA.
DE Human protein sequence SEQ ID NO:15600.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 6.1%; Score 85.5; DB 4; Length 545;
Best Local Similarity 23.0%; Pred. No. 3.3;
RESULT 851
ID AAY82460 standard; protein; 579 AA.
DE Human SM-11044-binding receptor protein SEQ ID NO:4.
PN WO200014266-A1.
PD 16-MAR-2000.
PA (SUMU) SUMITOMO PHARM CO LTD.
Query Match 6.1%; Score 85.5; DB 3; Length 579;
Best Local Similarity 23.0%; Pred. No. 3.6;
RESULT 852
ID AAY82459 standard; protein; 582 AA.
DE Human SM-11044-binding receptor protein SEQ ID NO:2.
PN WO200014266-A1.
PD 16-MAR-2000.
PA (SUMU) SUMITOMO PHARM CO LTD.
Query Match 6.1%; Score 85.5; DB 3; Length 582;
Best Local Similarity 23.0%; Pred. No. 3.6;
RESULT 853
ID ABB69104 standard; protein; 700 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 34104.
PN WO20011042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 6.1%; Score 85.5; DB 4; Length 700;
Best Local Similarity 19.7%; Pred. No. 4.6;
RESULT 854
ID AEB15131 standard; protein; 265 AA.
DE C glutamicum metabolic pathway regulatory (MR) protein SeqID46.
PN US2005153402-A1.
PD 14-JUL-2005.
PA (BADI) BASF AG.
Query Match 6.1%; Score 85; DB 9; Length 265;
Best Local Similarity 24.1%; Pred. No. 1.4;
RESULT 855
ID ABU34786 standard; protein; 338 AA.
DE Protein encoded by Prokaryotic essential gene #20313.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.1%; Score 85; DB 6; Length 338;
Best Local Similarity 23.1%; Pred. No. 1.9;
RESULT 856
ID ABU36544 standard; protein; 338 AA.
DE Protein encoded by Prokaryotic essential gene #22071.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.1%; Score 85; DB 6; Length 338;
Best Local Similarity 23.1%; Pred. No. 1.9;
RESULT 857
ID AAG90802 standard; protein; 419 AA.
DE C glutamicum protein fragment SEQ ID NO: 4556.
PN EPI108790-A2.
PD 20-JUN-2001.
PA (KIOW) KYOWA HAKKO KOGYO KK.
Query Match 6.1%; Score 85; DB 4; Length 419;
Best Local Similarity 24.1%; Pred. No. 2.6;
RESULT 858
ID AAE20418 standard; protein; 419 AA.
DE Corynebacterium glutamicum CHRS protein.
PN WO200220572-A2.
PD 14-MAR-2002.

PA (DEGS) DEGUSSA AG.
Query Match 6.1%; Score 85; DB 5; Length 419;
Best Local Similarity 24.1%; Pred. No. 2.6;
RESULT 859
ID AEB15129 standard; protein; 419 AA.
DE C glutamicum metabolic pathway regulatory (MR) protein SeqID44.
PN US2005153402-A1.
PD 14-JUL-2005.
PA (BADI) BASF AG.
Query Match 6.1%; Score 85; DB 9; Length 419;
Best Local Similarity 24.1%; Pred. No. 2.6;
RESULT 860
ID ABB55143 standard; protein; 443 AA.
DE Lactococcus lactis protein ysfC.
PN FR2807446-A1.
PD 12-OCT-2001.
PA (INRG) INRA INST NAT RECH AGRONOMIQUE.
Query Match 6.1%; Score 85; DB 5; Length 443;
Best Local Similarity 24.4%; Pred. No. 2.8;
RESULT 861
ID AAU78998 standard; protein; 498 AA.
DE Mouse Rh type C gene (RHCG) protein.
PN WO200220719-A2.
PD 14-MAR-2002.
PA (NYBL-) NEW YORK BLOOD CENT INC.
Query Match 6.1%; Score 85; DB 5; Length 498;
Best Local Similarity 20.2%; Pred. No. 3.3;
RESULT 862
ID ADE56874 standard; protein; 1166 AA.
DE Rat Protein Q03343, SEQ ID NO 2729.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GHEO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 6.1%; Score 85; DB 7; Length 1166;
Best Local Similarity 19.8%; Pred. No. 11;
RESULT 863
ID AAB02010 standard; protein; 1180 AA.
DE Type VI adenylyl cyclase.
PN US6107076-A.
PD 22-AUG-2000.
PA (TEXA) UNIV TEXAS SYSTEM.
Query Match 6.1%; Score 85; DB 3; Length 1180;
Best Local Similarity 19.8%; Pred. No. 11;
RESULT 864
ID ADH88320 standard; protein; 296 AA.
DE Enterococcus faecalis polypeptide #2800.
PN US6617156-B1.
PD 09-SEP-2003.
PA (DOUC) DOUCETTE-STAMM L A.
PA (BUSH) BUSH D.
Query Match 6.1%; Score 84.5; DB 7; Length 296;
Best Local Similarity 25.2%; Pred. No. 1.8;
RESULT 865
ID ABM68417 standard; protein; 324 AA.
DE Photorhabdus luminescens protein sequence #1514.
PN WO200294867-A2.
PD 28-NOV-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 6.1%; Score 84.5; DB 6; Length 324;
Best Local Similarity 23.8%; Pred. No. 2.1;
RESULT 866
ID AAY07771 standard; protein; 356 AA.
DE Human secreted protein fragment encoded from gene 28.
PN WO9909155-A1.
PD 25-FEB-1999.
PA (HUNA-) HUMAN GENOME SCI INC.
Query Match 6.1%; Score 84.5; DB 2; Length 356;
Best Local Similarity 19.8%; Pred. No. 2.4;
RESULT 867
ID ABG75197 standard; protein; 408 AA.
DE Wheat homogentisate geranylgeranyl transferase.

PN WO2003082899-A2.
PD 09-OCT-2003.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 6.1%; Score 84.5; DB 7; Length 408;
Best Local Similarity 25.3%; Pred. No. 2.9;
RESULT 868
ID AAG46717 standard; protein; 446 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 58803.
PD 06-SEP-2000.
Query Match 6.1%; Score 84.5; DB 3; Length 446;
Best Local Similarity 19.0%; Pred. No. 3.2;
RESULT 869
ID AAY95015 standard; protein; 453 AA.
DE Human secreted protein vc61_1, SEQ ID NO:70.
PD 02-MAR-2000.
PA (ALPH-) ALPHAGEN INC.
Query Match 6.1%; Score 84.5; DB 3; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 870
ID AAG5236 standard; protein; 453 AA.
DE Protein tyrosine kinase 50.
PN CN1298944-A.
PD 13-JUN-2001.
PA (BODA-) BODAO GENE TECHNOLOGY CO LTD SHANGHAI.
Query Match 6.1%; Score 84.5; DB 4; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 871
ID AAU29065 standard; protein; 453 AA.
DE Human PRO polypeptide sequence #42.
PN WO200169848-A2.
PD 20-SEP-2001.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 4; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 872
ID RAM39489 standard; protein; 453 AA.
DE Human polypeptide SEQ ID NO 2634.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.1%; Score 84.5; DB 4; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 873
ID AAB65170 standard; protein; 453 AA.
DE Human PRO732 (UNQ396) protein sequence SEQ ID NO:73.
PN WO200073454-A1.
PD 07-DEC-2000.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 4; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 874
ID ABB90299 standard; protein; 453 AA.
DE Human polypeptide SEQ ID NO 2675.
PN WO200190304-A2.
PD 29-NOV-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.1%; Score 84.5; DB 5; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 875
ID ABU58441 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003027272-A1.
PD 06-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 876
ID ABU87989 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003032127-A1.
PD 13-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 877
ID ABU84304 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003032112-A1.
PD 13-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 878
ID ABR66178 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003027278-A1.
PD 06-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 879
ID ABR65568 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003036159-A1.
PD 20-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 880
ID ABU99508 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003040070-A1.
PD 27-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 881
ID ABU57985 standard; protein; 453 AA.
DE Human PRO polypeptide #17.
PN US2003027163-A1.
PD 06-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 882
ID ABU59063 standard; protein; 453 AA.
DE Novel human secreted or transmembrane protein PRO732.
PN US2002132252-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 883
ID ABU82575 standard; protein; 453 AA.
DE Human secreted/transmembrane protein PRO732.
PN US2003032023-A1.
PD 13-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 884
ID ABU82747 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003032113-A1.
PD 13-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 885
ID ABU99868 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003036147-A1.
PD 20-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 886
ID ABR68117 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003027264-A1.
PD 06-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 887

ID ABU60494 standard; protein; 453 AA.
DE Human secreted/transmembrane protein, #24.
PN US2002160384-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 888
ID ABU96170 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003036144-A1.
PD 20-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 889
ID ABU92601 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003036149-A1.
PD 20-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 890
ID ABO08678 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003044923-A1.
PD 06-MAR-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 891
ID ABO02730 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003040062-A1.
PD 27-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 892
ID ABR74884 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003040056-A1.
PD 27-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 893
ID ABR94646 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003044926-A1.
PD 06-MAR-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 894
ID ABU13876 standard; protein; 453 AA.
DE Human PRO732 polypeptide.
PN US2002103125-A1.
PD 01-AUG-2002.
PA (GETH) GENENTECH LTD.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 895
ID ABU85619 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003036140-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 896
ID ABU98779 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003013153-A1.
PD 16-JAN-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 897

ID ABU97994 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003017544-A1.
PD 23-JAN-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 898
ID ABU91700 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003027277-A1.
PD 06-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 899
ID ABU89393 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003036141-A1.
PD 20-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 900
ID ABU86234 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003036146-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 901
ID ABU67447 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003036162-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 902
ID ABU80475 standard; protein; 453 AA.
DE Human PRO protein #42.
PN US2003036137-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 903
ID ABU72461 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003030351-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 904
ID ABR99393 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003040063-A1.
PD 27-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 905
ID ABR98783 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003040064-A1.
PD 27-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 906
ID ABO16306 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003027267-A1.
PD 06-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;

RESULT 907
ID ABR92206 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003036160-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 908
ID ABO18847 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003044925-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 909
ID ABR78268 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003054474-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 910
ID ABO00143 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003032114-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 911
ID ABO00147 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003036124-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 912
ID ABO11475 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003036124-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 913
ID ABO02120 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003040054-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 914
ID ABU88694 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003036133-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 915
ID ABU83389 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003036134-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 916
ID ABO06190 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003022294-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 917
ID ABR59226 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003027266-A1.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003027275-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 918
ID ABO09288 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003027324-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 919
ID ABO19152 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003036118-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 920
ID ABO11170 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003036123-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 921
ID ABR66788 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003036148-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 922
ID ABO16001 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003040060-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 923
ID ABO13707 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003044916-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 924
ID ABU65610 standard; protein; 453 AA.
DE Human secreted/transmembrane protein, SEQ ID 84.
PN US2003036156-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 925
ID ABO07458 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003032117-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 926
ID ABO03645 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003036128-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 927
ID ABR67093 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003027266-A1.

PD 06-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 928
ID ABO15696 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003054483-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 929
ID ABUS5977 standard; protein; 453 AA.
DE Human secreted/transmembrane protein, PRO732.
PN US2003022298-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 930
ID ABUS65305 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003032102-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 931
ID ABUS9250 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003036117-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 932
ID ABU71153 standard; protein; 453 AA.
DE Human PRO732 protein.
PN US2003036143-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 933
ID ABO07763 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003032138-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 934
ID ABR70004 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003032130-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 935
ID ABR69337 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003036132-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 936
ID ABO01478 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003008353-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 937
ID ABUS1280 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003017542-A1.

PD 23-JAN-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 938
ID ABR60077 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003032137-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 939
ID ABR67812 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003027269-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 940
ID ABR65200 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003027268-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 941
ID ABR68422 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003027274-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 942
ID ABR71834 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003032135-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 943
ID ABUS9210 standard; protein; 453 AA.
DE Human secreted/transmembrane protein, #24.
PN US2003027162-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 944
ID ABUS5314 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003022295-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 945
ID ABUS9004 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003022297-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 946
ID ABUS3084 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003032105-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 947
ID ABUS9490 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003032123-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;

Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 948
ID ABU90488 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003032108-A1.
PD 13-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 949
ID ABU83999 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003032111-A1.
PD 13-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 950
ID ABU93650 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003032119-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 951
ID ABO25907 standard; protein; 453 AA.
DE Human PRO732 polypeptide.
PN US2002127576-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 952
ID ABR64895 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003027263-A1.
PD 06-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 953
ID ABR68727 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003027271-A1.
PD 06-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 954
ID ABO06543 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003036125-A1.
PD 20-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 955
ID ABR99088 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003040068-A1.
PD 27-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 956
ID ABU56972 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003027280-A1.
PD 06-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 957
ID ABU85924 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003022300-A1.
PD 30-JAN-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 958
ID ABU82211 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003036136-A1.
PD 20-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 959
ID ABU87222 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003036138-A1.
PD 20-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 960
ID ABU83694 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003032109-A1.
PD 13-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 961
ID ABO08068 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003040066-A1.
PD 27-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 962
ID ABU81779 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003032104-A1.
PD 13-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 963
ID ABU65943 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003036157-A1.
PD 20-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 964
ID ABR59772 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003032120-A1.
PD 13-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 965
ID ABU93960 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003036155-A1.
PD 20-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 966
ID ABU99813 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003022296-A1.
PD 30-JAN-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 967
ID ABR66483 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003027281-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 968
ID ABR90901 standard; protein; 453 AA.

DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003040058-A1.
PD 27-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 969
ID ABUS8916 standard; protein; 453 AA.
DE Human secreted/transmembrane protein, #24.
PN US2002142961-A1.
PD 03-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 970
ID ABUS94328 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003017540-A1.
PD 23-JAN-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 971
ID ABU79210 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003032106-A1.
PD 13-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 972
ID ABUS6539 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003032129-A1.
PD 13-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 973
ID ABUS6844 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003032131-A1.
PD 13-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 974
ID ABUS94633 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003032103-A1.
PD 13-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 975
ID ABO04560 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003032107-A1.
PD 13-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 976
ID ABR70309 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003032139-A1.
PD 13-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 977
ID ABUS2294 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003032187-A1.
PD 30-JAN-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 978
ID ABUS8474 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003022301-A1.

PD 30-JAN-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 979
ID ABR65873 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003036165-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 980
ID ABR64590 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003027262-A1.
PD 06-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 981
ID ABUS9359 standard; protein; 453 AA.
DE Novel human secreted or transmembrane protein PRO1120.
PN US2003027985-A1.
PD 06-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 982
ID ABU79515 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003032110-A1.
PD 13-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 983
ID ABUS2906 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003036142-A1.
PD 20-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 984
ID ABUS5865 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003036145-A1.
PD 20-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 985
ID ABUS1085 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003036154-A1.
PD 20-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 986
ID ABUS0178 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003036153-A1.
PD 20-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 987
ID ABO09593 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003044931-A1.
PD 06-MAR-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 988
ID ABO10865 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003036150-A1.
PD 20-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;

Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 989
ID ABR70919 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003040069-A1.
PD 27-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 990
ID ABU87527 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US200302293-A1.
PD 30-JAN-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 991
ID ABU91395 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003032128-A1.
PD 13-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 992
ID ABU84609 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003032116-A1.
PD 13-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 993
ID ABR69699 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003032122-A1.
PD 13-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 994
ID ABU80076 standard; protein; 453 AA.
DE Human PRO protein #42.
PN US2003036139-A1.
PD 20-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 995
ID ABU92125 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003017476-A1.
PD 23-JAN-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 996
ID ABU93345 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003017541-A1.
PD 23-JAN-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 997
ID ABO09898 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003017543-A1.
PD 23-JAN-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 998
ID ABO08983 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003036152-A1.
PD 20-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 999
ID ABU10831 standard; protein; 453 AA.

DE Human PRO polypeptide #17.
PN US2002123463-A1.
PD 05-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1000
ID ABU10551 standard; protein; 453 AA.
DE Human secreted/transmembrane protein #42.
PN US2002127584-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1001
ID ABU81583 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US200217164-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1002
ID ABU95560 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003032115-A1.
PD 13-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1003
ID ABU96769 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003032140-A1.
PD 13-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1004
ID ABR70614 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003040076-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1005
ID ABO04965 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003008352-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1006
ID ABO08373 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003044922-A1.
PD 06-MAR-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1007
ID ABU88522 standard; protein; 453 AA.
DE Human secreted and transmembrane polypeptide PRO732.
PN US2002197615-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1008
ID ABO34036 standard; protein; 453 AA.
DE Human PRO732 polypeptide.
PN US2003017981-A1.
PD 23-JAN-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;

Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1009
ID ABO05580 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US20030321118-A1.
PD 13-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1010
ID ABR73969 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003036135-A1.
PD 20-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1011
ID ABR95561 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003054455-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1012
ID ABR80858 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003049741-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1013
ID ABR81163 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003049743-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1014
ID ABM00859 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003049769-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1015
ID ABR88461 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068743-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1016
ID ABM77282 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003054479-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1017
ID ABO28766 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068685-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1018
ID ABO31511 standard; protein; 453 AA.

DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068725-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1019
ID ABM07928 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068752-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1020
ID ABO40408 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068682-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1021
ID ABO35833 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003068701-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1022
ID ABO43972 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003068755-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1023
ID ADA77836 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003073180-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1024
ID ABM24767 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003104539-A1.
PD 05-JUN-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1025
ID ABO03035 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003036131-A1.
PD 20-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1026
ID ABR90291 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003040075-A1.
PD 27-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1027
ID ABM17205 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003054459-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1028
ID ABR94951 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003044930-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1029
ID ABR95256 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003040071-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1030
ID ABO21494 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003054471-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1031
ID ABR97758 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003064452-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1032
ID ABR87546 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068705-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1033
ID ABM77587 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003054473-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1034
ID ABM27817 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003064440-A1.
PD 03-APR-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1035
ID ABM06098 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068704-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1036
ID ABM03604 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068722-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1037
ID ABO27546 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003073183-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1038
ID ABM26292 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003104549-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1039
ID ABO48074 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003049749-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1040
ID ABR92816 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003064462-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1041
ID ABO24577 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003065159-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1042
ID ADA37584 standard; protein; 453 AA.
DE Human secreted/transmembrane protein PRO732.
PN US2003008297-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1043
ID ABM11588 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003064447-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1044
ID ABM02689 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003073184-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1045
ID ABM15985 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003064463-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1046
ID ABO27546 standard; protein; 453 AA.

DE Human secreted/transmembrane protein (PRO) #42.
PD US2003064451-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1047
ID BM29037 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PD US2003058721-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1048
ID ABM07013 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PD US2003068699-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1049
ID ABM21107 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PD US2003068707-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1050
ID ABM09453 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PD US2003073175-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1051
ID ABO41323 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PD US2003068695-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1052
ID ABO36138 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PD US2003068703-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1053
ID ABO43667 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PD US2003058732-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1054
ID ABM76367 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PD US2003082717-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1055
ID ABM76063 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PD US2003104548-A1.

PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1056
ID ABM25682 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PD US2003104542-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1057
ID ABM25987 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PD US2003104543-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1058
ID ADA21270 standard; protein; 453 AA.
DE Human secreted/transmembrane polypeptide PRO732.
PD US2003054404-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1059
ID ABO03340 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PD US2003036127-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1060
ID ABO02425 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PD US2003040061-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1061
ID ABR90596 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PD US2003036130-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1062
ID ABR73664 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PD US2003054468-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1063
ID ABO16916 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PD US2003054470-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1064
ID ABR94341 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PD US2003044917-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1065
ID ABR75848 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PD US2003044929-A1.

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PD 06-MAR-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1066
ID ABR71224 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003059880-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1067
ID ABR93121 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003064465-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1068
ID ABR93426 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003054478-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1069
ID ADA10057 standard; protein; 453 AA.
DE Human secreted/transmembrane protein, PRO732.
PN US2003059831-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1070
ID ABR87851 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003088718-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1071
ID ABO27851 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003064454-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1072
ID ABO29986 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003064461-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1073
ID ABO33195 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003068724-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1074
ID ABO4883 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068727-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1075
ID ABO4843 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068772-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1076
ID ABO36443 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068714-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1077
ID ABO3528 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003068758-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1078
ID ABO39493 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068776-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1079
ID ABM10368 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003069407-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1080
ID ABM11893 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003104555-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1081
ID ABO52039 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003049768-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1082
ID ABO52344 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003049771-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1083
ID ABO23662 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003032134-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1084
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PN ADAL7601 standard; protein; 453 AA.
DE Human PRO732 polypeptide.
PD US2003054987-A1.
PD 20-MAR-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1085
ID ABR97148 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PD US2003054481-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1086
ID ABR86936 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PD US2003049778-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1087
ID ABM10978 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PD US2003049782-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1088
ID ABM28122 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PD US2003054476-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1089
ID ABO32121 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PD US2003068733-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1090
ID ABM15248 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PD US2003068692-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1091
ID ABM06403 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PD US2003068709-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1092
ID ABM04214 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PD US2003068716-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1093
ID ABM22327 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.

PN US2003068740-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1094
ID ABM07623 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PD US2003068751-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1095
ID ABO40713 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PD US2003068684-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1096
ID ABM35360 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PD US2003073179-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1097
ID ABM33123 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PD US2003087374-A1.
PD 08-MAY-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1098
ID ABO52649 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PD US2003049773-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1099
ID ABO50209 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PD US2003049777-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1100
ID ABU99203 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PD US2003040055-A1.
PD 27-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1101
ID ABO04255 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PD US2003036164-A1.
PD 20-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1102
ID ABO05885 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PD US2003040074-A1.
PD 27-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;

RESULT 1103
ID ABM18425 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003054480-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1104
ID ADA27709 standard; protein; 453 AA.
DE Human secreted/transmembrane protein PRO732.
PN US2003054359-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1105
ID ABR97453 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003059885-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1106
ID ABR80553 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003049740-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1107
ID ABM01164 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003049770-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1108
ID ABR88766 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003073169-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1109
ID ABM13418 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003064457-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1110
ID ABM20802 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068711-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1111
ID ABO41933 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003049745-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1112
ID ABO42543 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.

PN US2003049751-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1113
ID ABM10063 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003067478-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1114
ID AB038578 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068773-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1115
ID ABM32818 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003073185-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1116
ID ABM22632 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003087373-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1117
ID ABM74843 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003096353-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1118
ID ADA79628 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003073173-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1119
ID ABR96233 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003054458-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1120
ID ABM02384 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003059886-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1121
ID ABR86326 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003049758-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;

RESULT 1122
ID ABR86631 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003049772-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1123
ID ABM16595 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003084448-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1124
ID ABM29647 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003064456-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1125
ID ABO29071 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068693-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1126
ID ABM23852 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068735-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1127
ID ABM23242 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068753-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1128
ID ABM22022 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068742-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1129
ID ABO37663 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068756-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1130
ID ABM28427 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003082715-A1.
PD 01-MAY-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
ID ABM28732 standard; protein; 453 AA.

DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003082716-A1.
PD 01-MAY-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1132
ID ABM66376 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068737-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1133
ID ABM75758 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003104547-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1134
ID ABM34038 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003096359-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1135
ID ABM34343 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003100061-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1136
ID ABO20274 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003032125-A1.
PD 13-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1137
ID ABO21189 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003054454-A1.
PD 20-MAR-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1138
ID ABO22104 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003054477-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1139
ID ABR96538 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003054460-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1140
ID ADA94289 standard; protein; 453 AA.
DE Human secreted/transmembrane protein PRO732.
PN US2003059832-A1.
PD 27-MAR-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;

Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1141
ID ABR95716 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003049753-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1142
ID ABR99698 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003049763-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1143
ID ABR00554 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003073172-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1144
ID ABR00249 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003073172-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1145
ID ABO23681 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068700-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1146
ID ABM23547 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068736-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1147
ID ABM29342 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068679-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1148
ID ABO38273 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068767-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1149
ID ABO45573 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003073182-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1150
ID ABM20497 standard; protein; 453 AA.

DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003104557-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1151
ID ADA81355 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003092121-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1152
ID ABO16611 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003027276-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1153
ID ABO18237 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003044920-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1154
ID ABO22664 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003027265-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1155
ID ABO22969 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003054461-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1156
ID ABR92511 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003064446-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1157
ID ABR81458 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003049744-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1158
ID ABM77892 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003049783-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1159
ID ABR99681 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003073171-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;

Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1160
ID ABM26597 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003032121-A1.
PD 13-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1161
ID ABM13723 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003064458-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1162
ID ABO28461 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003064460-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1163
ID ABO30291 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003064464-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1164
ID ABM07318 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068702-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1165
ID ABM03909 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068734-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1166
ID ABO37053 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068719-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1167
ID ABO41628 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068729-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1168
ID ABO35223 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003068738-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1169

ID ABM25072 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003104540-A1.
PD 05-JUN-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1170
ID ABO47464 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003049742-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1171
ID ABO47769 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003049747-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1172
ID ABO48379 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003049750-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1173
ID ABO51429 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003049766-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1174
ID ABO51734 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003049767-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1175
ID ABO50514 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003049779-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1176
ID ABR79638 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003040059-A1.
PD 27-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1177
ID ABM16900 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003040078-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1178
ID ABO17932 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003044918-A1.

PD 06-MAR-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1179
ID ABO20884 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003032132-A1.
PD 13-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1180
ID ABR96843 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003054452-A1.
PD 20-MAR-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1181
ID ADA38514 standard; protein; 453 AA.
DE Human secreted/transmembrane protein PRO732.
PN US2003059780-A1.
PD 27-MAR-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1182
ID ABM12198 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003064445-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1183
ID ABM16290 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003064449-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1184
ID ABM24157 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003064441-A1.
PD 03-APR-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1185
ID ABM14638 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003086695-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1186
ID ABM04519 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068712-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1187
ID ABM06708 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068730-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1188
ID ABM09148 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003073174-A1.
PD 17-APR-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1189
ID ABO39188 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068775-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1190
ID ABM75453 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003104545-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1191
ID ABM25377 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003104541-A1.
PD 05-JUN-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1192
ID ABM19887 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003104554-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1193
ID ABO46793 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003049762-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1194
ID ABO47098 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003049765-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1195
ID ADA83153 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003049752-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1196
ID ABR71529 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003032133-A1.
PD 13-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1197
ID ABR72139 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003032136-A1.
PD 13-FEB-2003.

Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1198
ID ABR98478 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003036129-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1199
ID ABO06848 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003040053-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1200
ID ABR4801 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003040057-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1201
ID ABR73359 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003054467-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1202
ID ABR76453 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003044932-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1203
ID ABR73054 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003027270-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1204
ID ABM18120 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003054469-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1205
ID ABO20579 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003032126-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1206
ID ABO25322 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003054463-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1207
ID ABO25627 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003054466-A1.
PD 20-MAR-2003.

PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1208
ID ABR94036 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003059879-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1209
ID ADA92635 standard; protein; 453 AA.
DE Human secreted/transmembrane protein PRO732.
PN US2003060407-A1.
PD 27-MAR-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1210
ID ABR79943 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003049738-A1.
PD 13-MAR-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1211
ID ABM11283 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003064469-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1212
ID ABO32890 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003064453-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1213
ID ABO30596 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003064466-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1214
ID ABO30901 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003064468-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1215
ID ABM27207 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068760-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1216
ID ABM29952 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068769-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1217
ID ABO25627 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003054466-A1.
PD 20-MAR-2003.

RESULT 1217
ID ABM05488 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003045700-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1218
ID ABM15553 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068698-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1219
ID ABM08538 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068759-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1220
ID ABO42238 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003049748-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1221
ID ABO37968 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068765-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1222
ID ABO45878 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003049754-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1223
ID ABM66681 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068688-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1224
ID ADB20196 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003082767-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1225
ID ABM19582 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003104552-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1226
ID ABO49294 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003049774-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1227
ID ABO49599 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003049775-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1228
ID ADA78448 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003073181-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1229
ID ABR88156 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068720-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1230
ID ABM26902 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068739-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1231
ID ABM03299 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068763-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1232
ID ABO39798 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068689-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1233
ID ABO49904 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003049776-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1234
ID ABO50819 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003049780-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1235
ID ABO05275 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.

PN US2003036126-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 453;
RESULT 1236
ID ABR74579 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003044924-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 453;
RESULT 1237
ID ABR77058 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003044927-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 453;
RESULT 1238
ID ABR17815 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003040072-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 453;
RESULT 1239
ID ABR95866 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003040073-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 453;
RESULT 1240
ID ABO21799 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003054475-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 453;
RESULT 1241
ID ABO19969 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003032124-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 453;
RESULT 1242
ID ABO24272 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003064467-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 453;
RESULT 1243
ID ABR86021 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003049759-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 453;
RESULT 1244
ID ABR10673 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003064455-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 453;
RESULT 1245
ID ABR76672 standard; protein; 453 AA.

DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003054465-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 453;
RESULT 1246
ID ABR89376 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003073170-A1.
PD 17-APR-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 453;
RESULT 1247
ID ABR12503 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003073176-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 453;
RESULT 1248
ID ABR05793 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068717-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 453;
RESULT 1249
ID ABO34918 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003068728-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 453;
RESULT 1250
ID ABR02994 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068764-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 453;
RESULT 1251
ID ABR18972 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003104550-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 453;
RESULT 1252
ID ABR19277 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003104551-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 453;
RESULT 1253
ID ABO46488 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003049761-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 453;
RESULT 1254
ID ABO48999 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003049757-A1.

PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 453;
Pred. No. 3.3;
RESULT 1255
ID ABR69032 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003027273-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 453;
Pred. No. 3.3;
RESULT 1256
ID ABR69071 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003036119-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 453;
Pred. No. 3.3;
RESULT 1257
ID ABR72444 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003036120-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 453;
Pred. No. 3.3;
RESULT 1258
ID ABR74274 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003036161-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 453;
Pred. No. 3.3;
RESULT 1259
ID ABO18542 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003044921-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 453;
Pred. No. 3.3;
RESULT 1260
ID ABR80248 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003049739-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 453;
Pred. No. 3.3;
RESULT 1261
ID ABM01469 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003059882-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 453;
Pred. No. 3.3;
RESULT 1262
ID ABM02079 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003059884-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 453;
Pred. No. 3.3;
RESULT 1263
ID ABR87241 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068687-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 453;
Pred. No. 3.3;
RESULT 1264
ID ABR87241 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068687-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 453;
Pred. No. 3.3;
RESULT 1265
ID ABM30562 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003064443-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 453;
Pred. No. 3.3;
RESULT 1266
ID ABM24462 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003064444-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 453;
Pred. No. 3.3;
RESULT 1267
ID ABO29376 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068697-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 453;
Pred. No. 3.3;
RESULT 1268
ID ABO31206 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068710-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 453;
Pred. No. 3.3;
RESULT 1269
ID ABM14333 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068686-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 453;
Pred. No. 3.3;
RESULT 1270
ID ABM09758 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003073178-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 453;
Pred. No. 3.3;
RESULT 1271
ID ABO38883 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068774-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 453;
Pred. No. 3.3;
RESULT 1272
ID ABM34648 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003104538-A1.
PD 05-JUN-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 453;
Pred. No. 3.3;
RESULT 1273
ID ABO51124 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.

PN US2003049781-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 453;
RESULT 1274
ID ABO03950 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003036158-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 453;
RESULT 1275
ID ABO10420 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003036151-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 453;
RESULT 1276
ID ABO53122 standard; protein; 453 AA.
DE Human secreted/transmembrane protein PRO732.
PN US2003044806-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 453;
RESULT 1277
ID ABR77663 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003040067-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 453;
RESULT 1278
ID ABR78873 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003054482-A1.
PD 20-MAR-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 453;
RESULT 1279
ID ABO23967 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003054482-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 453;
RESULT 1280
ID ABR93731 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003054457-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 453;
RESULT 1281
ID ABO01774 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003059883-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 453;
RESULT 1282
ID ABR78197 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003049764-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 453;
RESULT 1283
ID ABR93733 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003096358-A1.
PD 22-MAY-2003.

ID ABR9986 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003073177-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 453;
RESULT 1284
ID ADA22196 standard; protein; 453 AA.
DE Human secreted/transmembrane polypeptide PRO732.
PN US2003040473-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 453;
RESULT 1285
ID ABM27512 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003064442-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 453;
RESULT 1286
ID ABM13113 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003064450-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 453;
RESULT 1287
ID ABO31816 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068731-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 453;
RESULT 1288
ID ABM14028 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068683-A1.
PD 10-APR-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 453;
RESULT 1289
ID ABM08233 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068754-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 453;
RESULT 1290
ID ABO40103 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068681-A1.
PD 10-APR-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 453;
RESULT 1291
ID ABM74538 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003096351-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 453;
RESULT 1292
ID ABM33733 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003096358-A1.
PD 22-MAY-2003.

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PA (GETH ) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1293
ID ABM20192 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003104556-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1294
ID ABO48684 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003049756-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1295
ID ABO22492 standard; protein; 453 AA.
DE Human secreted/transmembrane protein PRO732.
PN US2003017982-A1.
PD 23-JAN-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1296
ID ABR72749 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003036122-A1.
PD 20-FEB-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1297
ID ABO15391 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003036121-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1298
ID ABR85106 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003040065-A1.
PD 27-FEB-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1299
ID ABO15086 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003044919-A1.
PD 06-MAR-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1300
ID ABO17221 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003040077-A1.
PD 27-FEB-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1301
ID ABM17510 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003044928-A1.
PD 06-MAR-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1302
ID ADA06362 standard; protein; 453 AA.
DE Human secreted/transmembrane PRO polypeptide #17.
PN US2003049638-A1.

PA (GETH ) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1303
ID ADA39055 standard; protein; 453 AA.
DE Human secreted/transmembrane protein PRO732.
PN US2003059782-A1.
PD 27-MAR-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1304
ID ABR85411 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003049746-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1305
ID ABM76977 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003054464-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1306
ID ABO28156 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003064459-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1307
ID ABM22937 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068757-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1308
ID ABM30257 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068723-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1309
ID ABM21717 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068741-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1310
ID ABM21412 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068744-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1311
ID ABM14943 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068766-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
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Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1312
ID ABO41018 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068694-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 453;
RESULT 1313
ID ABO36748 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068715-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 453;
RESULT 1314
ID ABO377358 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068726-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 453;
RESULT 1315
ID ABM75148 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003104544-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 453;
RESULT 1316
ID ABM33428 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003096357-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 453;
RESULT 1317
ID ABO46183 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003049760-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 453;
RESULT 1318
ID ADA82519 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003049755-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 453;
RESULT 1319
ID ADB96081 standard; protein; 453 AA.
DE Human PRO polypeptide #17.
PN US2003054403-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 453;
RESULT 1320
ID ABM31782 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068680-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 453;
RESULT 1321
ID ABM31172 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068762-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 453;
RESULT 1322
ID ADB85827 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003054472-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 453;
RESULT 1323
ID ABM32087 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068708-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 453;
RESULT 1324
ID ABM32392 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068713-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 453;
RESULT 1325
ID ABM31477 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068761-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 453;
RESULT 1326
ID ABM30867 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068771-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 453;
RESULT 1327
ID ADC57553 standard; protein; 453 AA.
DE Human PRO polypeptide #17.
PN US2003027754-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 453;
RESULT 1328
ID ADC54917 standard; protein; 453 AA.
DE Human PRO polypeptide #17.
PN US2003045463-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 453;
RESULT 1329
ID ADC11784 standard; protein; 453 AA.
DE Human secreted/transmembrane protein PRO732.
PN US2003049681-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 453;
RESULT 1330
ID ADC56206 standard; protein; 453 AA.
DE Human PRO polypeptide #17.
PN US2003064375-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 453;

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Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1331
ID ADC07261 standard; protein; 453 AA.
DE Human secreted/transmembrane protein PRO732.
PN US2003068647-A1.
PD 10-APR-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1332
ID ADC11251 standard; protein; 453 AA.
DE Human secreted/transmembrane protein PRO732.
PN US2003069403-A1.
PD 10-APR-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1333
ID ADC14373 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003082546-A1.
PD 01-MAY-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1334
ID ADD07905 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003068623-A1.
PD 10-APR-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1335
ID ADC81730 standard; protein; 453 AA.
DE Human PRO polypeptide #17.
PN US2003083461-A1.
PD 01-MAY-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1336
ID ADD07372 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2002193299-A1.
PD 19-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1337
ID ADC77580 standard; protein; 453 AA.
DE Human TMS2 amino acid sequence.
PN WO2003068829-A2.
PD 14-AUG-2003.
PA (DISC-) DISCOVERY GENOMICS INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1338
ID ADC82263 standard; protein; 453 AA.
DE Human PRO polypeptide #17.
PN US2003059833-A1.
PD 27-MAR-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1339
ID ADD05557 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003087376-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1340
ID ADD08443 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003073090-A1.
PD 17-APR-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;

Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1341
ID ADD06692 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2002193300-A1.
PD 19-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1342
ID ADC82939 standard; protein; 453 AA.
DE Human PRO polypeptide #17.
PN US2003059783-A1.
PD 27-MAR-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1343
ID ADD55046 standard; protein; 453 AA.
DE Human PRO polypeptide #17.
PN US2003077593-A1.
PD 24-APR-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1344
ID ADD56004 standard; protein; 453 AA.
DE Human PRO polypeptide #17.
PN US2003077594-A1.
PD 24-APR-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1345
ID ADD54442 standard; protein; 453 AA.
DE Human PRO polypeptide #17.
PN US2002132253-A1.
PD 19-SEP-2002.
PA (GETH ) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1346
ID ADE26596 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003087304-A1.
PD 08-MAY-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1347
ID ADE26063 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003087305-A1.
PD 08-MAY-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1348
ID ADF67000 standard; protein; 453 AA.
DE Human PRO732 amino acid sequence SEQ ID NO:73.
PN US2002198148-A1.
PD 26-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1349
ID ADG02552 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003207397-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1350
ID ADG01259 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003207399-A1.
PD 06-NOV-2003.
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PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1351
ID ADF95434 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003207398-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1352
ID ADG12249 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003207392-A1.
PD 06-NOV-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1353
ID ADH08909 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003207395-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1354
ID ADI35254 standard; protein; 453 AA.
DE Human PRO polypeptide #17.
PN US2003050457-A1.
PD 13-MAR-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1355
ID ADH99746 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003049682-A1.
PD 13-MAR-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1356
ID ADL32690 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003207396-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1357
ID ADM30224 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003073813-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1358
ID ADE74221 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003211572-A1.
PD 13-NOV-2003.
Query Match 6.1%; Score 84.5; DB 8; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1359
ID ADE74833 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003211574-A1.
PD 13-NOV-2003.
Query Match 6.1%; Score 84.5; DB 8; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1360
ID ADF35199 standard; protein; 453 AA.
DE Human PRO732 polypeptide.

PN US2003194760-A1.
PD 16-OCT-2003.
Query Match 6.1%; Score 84.5; DB 8; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1361
ID ADG11449 standard; protein; 453 AA.
DE Human PRO732 polypeptide.
PN US2003228655-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 8; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1362
ID ADF96046 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003215909-A1.
PD 20-NOV-2003.
Query Match 6.1%; Score 84.5; DB 8; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1363
ID ADG04317 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003215912-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 8; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1364
ID ADG00477 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003215910-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 8; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1365
ID ADG82733 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003215910-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 8; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1366
ID ADH26014 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003068770-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 8; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1367
ID ADH19319 standard; protein; 453 AA.
DE Human secreted/transmembrane protein PRO732.
PN US2003228656-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 8; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1368
ID ADH32983 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003068768-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 8; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1369
ID ADH20812 standard; protein; 453 AA.
DE Human secreted/transmembrane protein PRO732.
PN US2003224358-A1.
PD 04-DEC-2003.
Query Match 6.1%; Score 84.5; DB 8; Length 453;

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Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1370
ID ADH19852 standard; protein; 453 AA.
DE Human secreted/transmembrane protein PRO732.
PN US2003219856-A1.
PD 27-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 8; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1371
ID ADJ54722 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2004023321-A1.
PD 05-FEB-2004.
PA (GETH ) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 8; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1372
ID ADJ64493 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2004038337-A1.
PD 26-FEB-2004.
PA (GETH ) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 8; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1373
ID ADM31389 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2004048334-A1.
PD 11-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 8; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1374
ID ADM36436 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2004053358-A1.
PD 18-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 8; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1375
ID ADM40241 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2004048335-A1.
PD 11-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 8; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1376
ID ADN37849 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2004091959-A1.
PD 13-MAY-2004.
PA (GETH ) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 8; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1377
ID ADR09184 standard; protein; 453 AA.
DE Human protein useful for treating neurological disease Seq 2690.
PN EP1447413-A2.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 6.1%; Score 84.5; DB 8; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1378
ID ARM80816 standard; protein; 453 AA.
DE Tumour-associated antigenic target (TAT) polypeptide PRO81457, SEQ:2102.
PN W02004030615-A2.
PD 15-APR-2004.
PA (GETH ) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 8; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1379
ID ADR99176 standard; protein; 453 AA.
DE KIAA1253 SEQ ID 182.
PN WO2004078035-A2.
PD 16-SEP-2004.
PA (FARB ) BAYER PHARM CORP.
Query Match 6.1%; Score 84.5; DB 8; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1380
ID ADV69528 standard; protein; 453 AA.
DE Human tyrosine kinase 50 amino acid sequence - SEQ ID 2.
PN CN1510134-A.
PD 07-JUL-2004.
PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
Query Match 6.1%; Score 84.5; DB 8; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1381
ID AEA38376 standard; protein; 453 AA.
DE Human secreted/transmembrane protein cDNA, #86.
PN US2005112725-A1.
PD 26-MAY-2005.
PA (GETH ) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 9; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1382
ID AED50079 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2005163766-A1.
PD 28-JUL-2005.
PA (GETH ) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 9; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1383
ID ADG10618 standard; protein; 472 AA.
DE Human STRA6-activating protein, SEQ ID NO:208.
PN WO200296943-A1.
PD 05-DEC-2002.
PA (ASAH ) ASAH KASEI KOGYO KK.
Query Match 6.1%; Score 84.5; DB 7; Length 472;
Best Local Similarity 19.8%; Pred. No. 3.5;
RESULT 1384
ID AAM41275 standard; protein; 477 AA.
DE Human polypeptide SEQ ID NO 6206.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.1%; Score 84.5; DB 4; Length 477;
Best Local Similarity 19.8%; Pred. No. 3.6;
RESULT 1385
ID AAG46716 standard; protein; 521 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 58802.
PN EP1033405-A2.
PD 06-SEP-2000.
PA (FARB ) BAYER AG.
Query Match 6.1%; Score 84.5; DB 3; Length 521;
Best Local Similarity 19.0%; Pred. No. 4;
RESULT 1386
ID ABB93783 standard; protein; 562 AA.
DE Herbicidically active polypeptide SEQ ID NO 2994.
PN WO200210210-A2.
PD 07-FEB-2002.
PA (FARB ) BAYER AG.
Query Match 6.1%; Score 84.5; DB 5; Length 562;
Best Local Similarity 19.6%; Pred. No. 4.5;
RESULT 1387
ID AAG46715 standard; protein; 571 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 58801.
PN EP1033405-A2.
PD 06-SEP-2000.
PA (FARB ) BAYER AG.
Query Match 6.1%; Score 84.5; DB 3; Length 571;
Best Local Similarity 19.0%; Pred. No. 4.5;
RESULT 1388
ID ADX95745 standard; protein; 600 AA.
DE Plant full length insert polypeptide seqid 58409.
PN US2004034888-A1.
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PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 6.1%; Score 84.5; DB 8; Length 600;
Best Local Similarity 23.0%; Pred. No. 4.9;
RESULT 1389
ID ADA36714 standard; protein; 241 AA.
DE Acinetobacter baumannii protein #3875.
PN US6562958-B1.
PD 13-MAY-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 6.0%; Score 84; DB 6; Length 241;
Best Local Similarity 22.8%; Pred. No. 1.6;
RESULT 1390
ID ABG61495 standard; protein; 318 AA.
DE Iron uptake ABC transporter polypeptide #2.
PN WO200234773-A2.
PD 02-MAY-2002.
PA (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
Query Match 6.0%; Score 84; DB 5; Length 318;
Best Local Similarity 24.4%; Pred. No. 2.3;
RESULT 1391
ID ABU02362 standard; protein; 318 AA.
DE S. pneumoniae type 4 strain protein from coding region #1940.
PN WO200277021-A2.
PD 03-OCT-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match 6.0%; Score 84; DB 6; Length 318;
Best Local Similarity 24.4%; Pred. No. 2.3;
RESULT 1392
ID ADZ10513 standard; protein; 403 AA.
DE P. gingivalis hypothetical protein SEQ ID 296.
PN WO2005019249-A2.
PD 03-MAR-2005.
PA (UYFL) UNIV FLORIDA.
Query Match 6.0%; Score 84; DB 9; Length 403;
Best Local Similarity 21.9%; Pred. No. 3.2;
RESULT 1393
ID ABG10541 standard; protein; 480 AA.
DE Novel human diagnostic protein #10532.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.0%; Score 84; DB 4; Length 480;
Best Local Similarity 20.5%; Pred. No. 4.1;
RESULT 1394
ID ADL04919 standard; protein; 506 AA.
DE M. catarrhalis protein #685.
PN US6673910-B1.
PD 06-JAN-2004.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 6.0%; Score 84; DB 8; Length 506;
Best Local Similarity 19.9%; Pred. No. 4.4;
RESULT 1395
ID ADS23392 standard; protein; 516 AA.
DE Bacterial polypeptide #12425.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 6.0%; Score 84; DB 8; Length 516;
Best Local Similarity 25.0%; Pred. No. 4.5;
RESULT 1396
ID ABO67632 standard; protein; 537 AA.
DE Klebsiella pneumoniae polypeptide seqid 14149.
PN US6610836-B1.
PD 26-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 6.0%; Score 84; DB 7; Length 537;
Best Local Similarity 18.7%; Pred. No. 4.8;
RESULT 1397
ID ABU38257 standard; protein; 575 AA.
DE Protein encoded by Prokaryotic essential gene #23784.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.0%; Score 84; DB 6; Length 575;
Best Local Similarity 20.3%; Pred. No. 5.2;
RESULT 1398
ID ABO73781 standard; protein; 602 AA.
DE Pseudomonas aeruginosa polypeptide #5956.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 6.0%; Score 84; DB 7; Length 602;
Best Local Similarity 20.3%; Pred. No. 5.6;
RESULT 1399
ID ABO70835 standard; protein; 720 AA.
DE Pseudomonas aeruginosa polypeptide #3010.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 6.0%; Score 84; DB 7; Length 720;
Best Local Similarity 21.8%; Pred. No. 7.1;
RESULT 1400
ID ABU32051 standard; protein; 1137 AA.
DE Protein encoded by Prokaryotic essential gene #17578.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.0%; Score 84; DB 6; Length 1137;
Best Local Similarity 18.6%; Pred. No. 13;
RESULT 1401
ID ABO67057 standard; protein; 1138 AA.
DE Klebsiella pneumoniae polypeptide seqid 13574.
PN US6610836-B1.
PD 26-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 6.0%; Score 84; DB 7; Length 1138;
Best Local Similarity 18.6%; Pred. No. 13;
RESULT 1402
ID ADT60220 standard; protein; 294 AA.
DE Plant polypeptide, SEQ ID 10297.
PN US2004216190-A1.
PD 28-OCT-2004.
PA (KOVA/) KOVALIC D K.
Query Match 6.0%; Score 83.5; DB 8; Length 294;
Best Local Similarity 25.4%; Pred. No. 2.4;
RESULT 1403
ID ABU37874 standard; protein; 295 AA.
DE Protein encoded by Prokaryotic essential gene #23401.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.0%; Score 83.5; DB 6; Length 295;
Best Local Similarity 21.6%; Pred. No. 2.4;
RESULT 1404
ID AEF12231 standard; protein; 308 AA.
DE Murine trace amine associated receptor 7b SEQ ID NO:50.
PN US2006009441-A1.
PD 12-JAN-2006.
PA (EBEL/) EBELING M.
PA (HOEN/) HOENER M.
PA (LIND/) LINDEMANN L.
Query Match 6.0%; Score 83.5; DB 10; Length 308;
Best Local Similarity 28.6%; Pred. No. 2.5;
RESULT 1405
ID ADV88472 standard; protein; 333 AA.

DE Streptococcus agalactiae protein sequence, SEQ ID 866.
PN FR2624074-A1.
PD 31-OCT-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 6.0%; Score 83.5; DB 8; Length 333;
Best Local Similarity 21.4%; Pred. No. 2.8;
RESULT 1406
ID ADV79725 standard; protein; 333 AA.
DE Streptococcus agalactiae protein, SEQ ID 866.
PN WO200292818-A2.
PD 21-NOV-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 6.0%; Score 83.5; DB 8; Length 333;
Best Local Similarity 21.4%; Pred. No. 2.8;
RESULT 1407
ID ADV81883 standard; protein; 333 AA.
DE Streptococcus agalactiae protein, SEQ ID 3024.
PN WO200292818-A2.
PD 21-NOV-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 6.0%; Score 83.5; DB 8; Length 333;
Best Local Similarity 21.4%; Pred. No. 2.8;
RESULT 1408
ID AAR97984 standard; protein; 618 AA.
DE DmORF1 potassium channel protein.
PN WO9613520-A1.
PD 09-MAY-1996.
PA (AMCY) AMERICAN CYANAMID CO.
Query Match 6.0%; Score 83.5; DB 2; Length 618;
Best Local Similarity 19.9%; Pred. No. 6.6;
RESULT 1409
ID AAU07616 standard; protein; 618 AA.
DE Drosophila melanogaster potassium ion channel ORF1 (DmORF1) protein.
PN WO200161006-A2.
PD 23-AUG-2001.
PA (BADI) BASF CORP.
Query Match 6.0%; Score 83.5; DB 4; Length 618;
Best Local Similarity 19.9%; Pred. No. 6.6;
RESULT 1410
ID ABG30123 standard; protein; 1027 AA.
DE Novel human diagnostic protein #30114.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.0%; Score 83.5; DB 4; Length 1027;
Best Local Similarity 19.8%; Pred. No. 13;
RESULT 1411
ID ABU28293 standard; protein; 1090 AA.
DE Protein encoded by Prokaryotic essential gene #13820.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.0%; Score 83.5; DB 6; Length 1090;
Best Local Similarity 18.5%; Pred. No. 14;
RESULT 1412
ID AAG44538 standard; protein; 250 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 55802.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.0%; Score 83; DB 3; Length 250;
Best Local Similarity 21.7%; Pred. No. 2.2;
RESULT 1413
ID AAG66371 standard; protein; 305 AA.
DE Human partial olfactory receptor-like protein OLF#2.
PN WO200155179-A2.
PD 02-AUG-2001.
PA (CURA-) CURAGEN CORP.
Query Match 6.0%; Score 83; DB 4; Length 305;
Best Local Similarity 20.6%; Pred. No. 2.8;
RESULT 1414
ID AAY85935 standard; protein; 318 AA.
DE S. pneumoniae derived protein #144.
PN WO9806734-A1.
PD 19-FEB-1998.
PA (SMIK) SMITHKLINE BEECHAM CORP.
Query Match 6.0%; Score 83; DB 2; Length 318;
Best Local Similarity 24.4%; Pred. No. 3;
RESULT 1415
ID ADK46461 standard; protein; 318 AA.
DE Streptococcus pneumoniae protein, Seq ID No 2976.
PN US6699703-B1.
PD 02-MAR-2004.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 6.0%; Score 83; DB 8; Length 318;
Best Local Similarity 24.4%; Pred. No. 3;
RESULT 1416
ID AAG71916 standard; protein; 319 AA.
DE Human olfactory receptor polypeptide, SEQ ID NO: 1597.
PN WO200127158-A2.
PD 19-APR-2001.
PA (DIGI-) DIGISCENTS.
PA (YEDA) YEDA RES & DEV CO LTD.
Query Match 6.0%; Score 83; DB 4; Length 319;
Best Local Similarity 20.6%; Pred. No. 3;
RESULT 1417
ID AAB46999 standard; protein; 321 AA.
DE Human OLFXY protein.
PN DE19937839-A1.
PD 15-FEB-2001.
PA (BRUE/) BRUESS M.
PA (BOEN/) BOENISCH H.
Query Match 6.0%; Score 83; DB 4; Length 321;
Best Local Similarity 20.6%; Pred. No. 3;
RESULT 1418
ID ABP95927 standard; protein; 321 AA.
DE Human GPCR polypeptide SEQ ID NO 664.
PN WO200216548-A2.
PD 28-FEB-2002.
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
Query Match 6.0%; Score 83; DB 5; Length 321;
Best Local Similarity 20.6%; Pred. No. 3;
RESULT 1419
ID ADU24127 standard; protein; 321 AA.
DE Human aspartic peptidase enzyme #19.
PN US2004219609-A1.
PD 04-NOV-2004.
PA (DAYA/) DAY A G.
PA (ESTE/) ESTELL D A.
PA (LYON/) LYONS E H.
PA (YAOJ/) YAO J.
Query Match 6.0%; Score 83; DB 8; Length 321;
Best Local Similarity 20.6%; Pred. No. 3;
RESULT 1420
ID ADR96441 standard; protein; 336 AA.
DE Novel S. pneumoniae protein sequence, SEQ ID 5076.
PN US6800744-B1.
PD 05-OCT-2004.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 6.0%; Score 83; DB 8; Length 336;
Best Local Similarity 24.4%; Pred. No. 3.2;
RESULT 1421
ID AEA60311 standard; protein; 336 AA.
DE Streptococcus pneumoniae ORF amino acid sequence SEQ ID NO:5076.
PN US2005136404-A1.
PD 23-JUN-2005.
PA (DOUC/) DOUCETTE-STAMM L A.
PA (BUSH/) BUSH D.
Query Match 6.0%; Score 83; DB 9; Length 336;
Best Local Similarity 24.4%; Pred. No. 3.2;
RESULT 1422
ID ABU43979 standard; protein; 355 AA.
DE Protein encoded by Prokaryotic essential gene #29506.
PN WO200277183-A2.

PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.0%; Score 83; DB 6; Length 355;
Best Local Similarity 23.0%; Pred. No. 3.5;
RESULT 1423
ID ABO62213 standard; protein; 417 AA.
DE Klebsiella pneumoniae polypeptide seqid 8730.
PN US6610836-B1.
PD 26-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 6.0%; Score 83; DB 7; Length 417;
Best Local Similarity 20.8%; Pred. No. 4.4;
RESULT 1424
ID AAY66647 standard; protein; 455 AA.
DE Membrane-bound protein PRO732.
PN WO9963088-A2.
PD 09-DEC-1999.
PA (GETH) GENENTECH INC.
Query Match 6.0%; Score 83; DB 3; Length 455;
Best Local Similarity 19.8%; Pred. No. 4.9;
RESULT 1425
ID AAB96670 standard; protein; 490 AA.
DE Putative P. abyssii succinyl-CoA synthetase #5.
PN FR2792651-A1.
PD 27-OCT-2000.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 6.0%; Score 83; DB 4; Length 490;
Best Local Similarity 23.6%; Pred. No. 5.5;
RESULT 1426
ID ABO70524 standard; protein; 542 AA.
DE Pseudomonas aeruginosa polypeptide #2699.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 6.0%; Score 83; DB 7; Length 542;
Best Local Similarity 20.2%; Pred. No. 6.3;
RESULT 1427
ID ADA33498 standard; protein; 632 AA.
DE Acinetobacter baumannii protein #659.
PN US6562958-B1.
PD 13-MAY-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 6.0%; Score 83; DB 6; Length 632;
Best Local Similarity 25.1%; Pred. No. 7.7;
RESULT 1428
ID ABB65640 standard; protein; 774 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 23712.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEXE) PE CORP NY.
Query Match 6.0%; Score 83; DB 4; Length 774;
Best Local Similarity 22.4%; Pred. No. 10;
RESULT 1429
ID AAU38963 standard; protein; 774 AA.
DE Drosophila G-protein coupled receptor, GCPR #41.
PN WO200170980-A2.
PD 27-SEP-2001.
PA (PEXE) PE CORP NY.
Query Match 6.0%; Score 83; DB 4; Length 774;
Best Local Similarity 22.4%; Pred. No. 10;
RESULT 1430
ID ADC35871 standard; protein; 774 AA.
DE Drosophila G protein coupled receptor seq id 43.
PN US2003092124-A1.
PD 15-MAY-2003.
PA (APPL-) APPLERA CORP.
Query Match 6.0%; Score 83; DB 7; Length 774;
Best Local Similarity 22.4%; Pred. No. 10;
RESULT 1431
ID AAE38199 standard; protein; 802 AA.
DE Fruit fly G-protein-coupled receptor (GPCR) protein #48.
PN WO2003052078-A2.

PD 26-JUN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 6.0%; Score 83; DB 7; Length 802;
Best Local Similarity 22.4%; Pred. No. 11;
RESULT 1432
ID ABP70924 standard; protein; 2159 AA.
DE Maize DEK1 from B73.
PN WO2003011015-A2.
PD 13-FEB-2003.
PA (PION-) PIONEER HI-BRED INT INC.
Query Match 6.0%; Score 83; DB 6; Length 2159;
Best Local Similarity 20.6%; Pred. No. 42;
RESULT 1433
ID ADT57399 standard; protein; 2159 AA.
DE Plant polypeptide, SEQ ID 7476.
PN US2004216190-A1.
PD 28-OCT-2004.
PA (KOVA/) KOVALIC D K.
Query Match 6.0%; Score 83; DB 8; Length 2159;
Best Local Similarity 20.6%; Pred. No. 42;
RESULT 1434
ID ADS43623 standard; protein; 391 AA.
DE Bacterial polypeptide #22053.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 5.9%; Score 82.5; DB 8; Length 391;
Best Local Similarity 23.2%; Pred. No. 4.6;
RESULT 1435
ID ABU28011 standard; protein; 395 AA.
DE Protein encoded by Prokaryotic essential gene #13538.
PN WO200271183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.9%; Score 82.5; DB 6; Length 395;
Best Local Similarity 19.7%; Pred. No. 4.6;
RESULT 1436
ID AAW21009 standard; protein; 461 AA.
DE H. pylori cell envelope transporter protein, hp5e11726orf7.
PN WO9640893-A1.
PD 19-DEC-1996.
PA (ASTR) ASTRA AB.
Query Match 5.9%; Score 82.5; DB 2; Length 461;
Best Local Similarity 21.5%; Pred. No. 5.7;
RESULT 1437
ID ABO69393 standard; protein; 492 AA.
DE Pseudomonas aeruginosa polypeptide #1568.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.9%; Score 82.5; DB 7; Length 492;
Best Local Similarity 19.1%; Pred. No. 6.3;
RESULT 1438
ID ADN18812 standard; protein; 596 AA.
DE Bacterial polypeptide #1465.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 5.9%; Score 82.5; DB 8; Length 596;
Best Local Similarity 20.6%; Pred. No. 8.1;
RESULT 1439
ID ABG06558 standard; protein; 875 AA.
DE Novel human diagnostic protein #6549.
PN WO200175067-A2.
PD 11-OCT-2001.

PA (HYSE-) HYSEQ INC.
 Query Match 5.9%; Score 82.5; DB 4; Length 875;
 Best Local Similarity 26.0%; Pred. No. 14;
 RESULT 1440
 ID ADJ69204 standard; protein; 1457 AA.
 DE Human heat mitochondrial protein as a therapeutic target SeqID1010.
 PN WO2003087768-A2.
 PD 23-OCT-2003.
 PA (MITO-) MITOKOR.
 PA (BUCK-) BUCK INST AGE RES.
 Query Match 5.9%; Score 82.5; DB 7; Length 1457;
 Best Local Similarity 26.0%; Pred. No. 28;
 RESULT 1441
 ID ADJ69205 standard; protein; 1457 AA.
 DE Human heat mitochondrial protein as a therapeutic target SeqID1011.
 PN WO2003087768-A2.
 PD 23-OCT-2003.
 PA (MITO-) MITOKOR.
 PA (BUCK-) BUCK INST AGE RES.
 Query Match 5.9%; Score 82.5; DB 7; Length 1457;
 Best Local Similarity 26.0%; Pred. No. 28;
 RESULT 1442
 ID ADJ58460 standard; protein; 1457 AA.
 DE BAB13458.1(P450G5) protein.
 PN WO2004011648-A2.
 PD 05-FEB-2004.
 PA (INPH-) INPHARMATICA LTD.
 Query Match 5.9%; Score 82.5; DB 8; Length 1457;
 Best Local Similarity 26.0%; Pred. No. 28;
 RESULT 1443
 ID ADC31246 standard; protein; 2548 AA.
 DE Human novel polypeptide sequence, SEQ ID NO:1328.
 PN WO2003029271-A2.
 PD 10-APR-2003.
 PA (HYSE-) HYSEQ INC.
 Query Match 5.9%; Score 82.5; DB 7; Length 2548;
 Best Local Similarity 26.0%; Pred. No. 60;
 RESULT 1444
 ID ABO84919 standard; protein; 219 AA.
 DE Human cancer-associated protein (CAP) HP07-069.
 PN WO2004058146-A2.
 PD 15-JUL-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 5.9%; Score 82; DB 8; Length 219;
 Best Local Similarity 22.1%; Pred. No. 2.3;
 RESULT 1445
 ID AAB87783 standard; protein; 299 AA.
 DE Rat T2R03 amino acid sequence SEQ ID NO:81.
 PN WO200118050-A2.
 PD 15-MAR-2001.
 PA (REGC-) UNIV CALIFORNIA.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 Query Match 5.9%; Score 82; DB 4; Length 299;
 Best Local Similarity 22.8%; Pred. No. 3.6;
 RESULT 1446
 ID ADJ84452 standard; protein; 299 AA.
 DE Rat T2R G-protein coupled receptor seq id 5.
 PN US2004038312-A1.
 PD 26-FEB-2004.
 PA (ZUKE/) ZUKER C S.
 PA (ADLE/) ADLER J E.
 PA (HOON/) HOON M.
 PA (RYBA/) RYBA N.
 PA (MOEL/) MOELLER K.
 Query Match 5.9%; Score 82; DB 8; Length 299;
 Best Local Similarity 22.8%; Pred. No. 3.6;
 RESULT 1447
 ID ADR29142 standard; protein; 299 AA.
 DE Taste receptor modulation-related rat T2R03 protein sequence SeqID81.
 PN WO2004069191-A2.
 PD 19-AUG-2004.
 PA (SENO-) SENOMYX INC.
 Query Match 5.9%; Score 82; DB 8; Length 299;

Best Local Similarity 22.8%; Pred. No. 3.6;
 RESULT 1448
 ID AAS10684 standard; protein; 356 AA.
 DE A. thaliana FUP1 protein.
 PN DE19907209-A1.
 PD 24-AUG-2000.
 PA (FROM/) FROMMER W.
 Query Match 5.9%; Score 82; DB 3; Length 356;
 Best Local Similarity 19.4%; Pred. No. 4.6;
 RESULT 1449
 ID ABB91157 standard; protein; 356 AA.
 DE Herbicidally active polypeptide SEQ ID NO 368.
 PN WO200210210-A2.
 PD 07-FEB-2002.
 PA (FARB-) BAYER AG.
 Query Match 5.9%; Score 82; DB 5; Length 356;
 Best Local Similarity 19.4%; Pred. No. 4.6;
 RESULT 1450
 ID ABU28157 standard; protein; 417 AA.
 DE Protein encoded by Prokaryotic essential gene #13684.
 PN WO20027183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Query Match 5.9%; Score 82; DB 6; Length 417;
 Best Local Similarity 27.1%; Pred. No. 5.7;
 RESULT 1451
 ID ADX68336 standard; protein; 440 AA.
 DE Plant full length insert polypeptide seqid 39179.
 PN US2004034888-A1.
 PD 19-FEB-2004.
 PA (LIUJ/) LIU J.
 PA (ZHOU/) ZHOU Y.
 PA (KOVA/) KOVALIC D K.
 PA (SCRE/) SCREEN S E.
 PA (TABA/) TABASKA J E.
 PA (CAOY/) CAO Y.
 Query Match 5.9%; Score 82; DB 8; Length 440;
 Best Local Similarity 24.4%; Pred. No. 6.1;
 RESULT 1452
 ID ADK16901 standard; protein; 465 AA.
 DE Nanoarchaeum equitans cancer-associated (CA) protein #426.
 PN WO2003093434-A2.
 PD 13-NOV-2003.
 PA (DIVE-) DIVERSA CORP.
 Query Match 5.9%; Score 82; DB 8; Length 465;
 Best Local Similarity 23.7%; Pred. No. 6.6;
 RESULT 1453
 ID ABO81608 standard; protein; 474 AA.
 DE Pseudomonas aeruginosa polypeptide #13783.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Query Match 5.9%; Score 82; DB 7; Length 474;
 Best Local Similarity 20.1%; Pred. No. 6.8;
 RESULT 1454
 ID ADY13455 standard; protein; 478 AA.
 DE Plant full length insert polypeptide seqid 69270.
 PN US2004034888-A1.
 PD 19-FEB-2004.
 PA (LIUJ/) LIU J.
 PA (ZHOU/) ZHOU Y.
 PA (KOVA/) KOVALIC D K.
 PA (SCRE/) SCREEN S E.
 PA (TABA/) TABASKA J E.
 PA (CAOY/) CAO Y.
 Query Match 5.9%; Score 82; DB 8; Length 478;
 Best Local Similarity 23.3%; Pred. No. 6.8;
 RESULT 1455
 ID ADN23219 standard; protein; 573 AA.
 DE Bacterial polypeptide #5872.
 PN US2003233675-A1.
 PD 18-DEC-2003.
 PA (CAOY/) CAO Y.

PA (HINK/) HINKLE G J. 5.9%; Score 82; DB 8; Length 573;
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 18.5%; Pred. No. 8.8;
Best Local Similarity 18.5%; Pred. No. 8.8;
RESULT 1456
ID ADN23218 standard; protein; 573 AA.
DE Bacterial polypeptide #5971.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 5.9%; Score 82; DB 8; Length 573;
Best Local Similarity 18.5%; Pred. No. 8.8;
RESULT 1457
ID ABU50193 standard; protein; 1139 AA.
DE Protein encoded by Prokaryotic essential gene #35720.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.9%; Score 82; DB 6; Length 1139;
Best Local Similarity 19.5%; Pred. No. 23;
RESULT 1458
ID AAE04312 standard; protein; 1167 AA.
DE Human modified cardiac adenylylase VI (ACVI) isoform.
PN WO200148164-A2.
PD 05-JUL-2001.
PA (REGC) UNIV CALIFORNIA.
Query Match 5.9%; Score 82; DB 4; Length 1167;
Best Local Similarity 20.2%; Pred. No. 23;
RESULT 1459
ID ABG32870 standard; protein; 1167 AA.
DE Chimeric Adenylylase isoform 6, AC-VI.
PN US2002103147-A1.
PD 01-AUG-2002.
PA (HAMM/) HAMMOND H K.
PA (INSE/) INSEL P A.
PA (PING/) PING P.
PA (POST/) POST S R.
PA (GAOM/) GAO M.
Query Match 5.9%; Score 82; DB 5; Length 1167;
Best Local Similarity 20.2%; Pred. No. 23;
RESULT 1460
ID AAW30599 standard; protein; 1168 AA.
DE Human type VI adenylylase.
PN WO9901547-A1.
PD 14-JAN-1999.
PA (CORT-) COR THERAPEUTICS INC.
Query Match 5.9%; Score 82; DB 2; Length 1168;
Best Local Similarity 20.2%; Pred. No. 23;
RESULT 1461
ID AAE04311 standard; protein; 1168 AA.
DE Human cardiac adenylylase VI (ACVI) isoform #2.
PN WO200148164-A2.
PD 05-JUL-2001.
PA (REGC) UNIV CALIFORNIA.
Query Match 5.9%; Score 82; DB 4; Length 1168;
Best Local Similarity 20.2%; Pred. No. 23;
RESULT 1462
ID ABG32869 standard; protein; 1168 AA.
DE Human Adenylylase isoform 6, AC-VI, #2.
PN US2002103147-A1.
PD 01-AUG-2002.
PA (HAMM/) HAMMOND H K.
PA (INSE/) INSEL P A.
PA (PING/) PING P.
PA (POST/) POST S R.
PA (GAOM/) GAO M.
Query Match 5.9%; Score 82; DB 5; Length 1168;

Best Local Similarity 20.2%; Pred. No. 23;
RESULT 1463
ID ADE56876 standard; protein; 1168 AA.
DE Human Protein O43306, SEQ ID NO 2731.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 5.9%; Score 82; DB 7; Length 1168;
Best Local Similarity 20.2%; Pred. No. 23;
RESULT 1464
ID ADQ98850 standard; protein; 1168 AA.
DE Antagonist of cell cycle progression polypeptide #140.
PN WO2004063362-A2.
PD 29-JUL-2004.
PA (CYCL-) CYCLACEL LTD.
Query Match 5.9%; Score 82; DB 8; Length 1168;
Best Local Similarity 20.2%; Pred. No. 23;
RESULT 1465
ID ADX98516 standard; protein; 1168 AA.
DE Human adenylate cyclase 6 (ADCV6) protein.
PN WO2005017121-A2.
PD 24-FEB-2005.
PA (EXEL-) EXELIXIS INC.
Query Match 5.9%; Score 82; DB 9; Length 1168;
Best Local Similarity 20.2%; Pred. No. 23;
RESULT 1466
ID ADK46612 standard; protein; 199 AA.
DE Streptococcus pneumoniae protein, Seq ID No 3127.
PN US6599703-B1.
PD 02-MAR-2004.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.9%; Score 81.5; DB 8; Length 199;
Best Local Similarity 20.2%; Pred. No. 2.3;
RESULT 1467
ID ABU02196 standard; protein; 205 AA.
DE S. pneumoniae type 4 strain protein from coding region #1774.
PN WO200277021-A2.
PD 03-OCT-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match 5.9%; Score 81.5; DB 6; Length 205;
Best Local Similarity 20.2%; Pred. No. 2.4;
RESULT 1468
ID AAY81546 standard; protein; 206 AA.
DE Streptococcus pneumoniae type 4 protein sequence #46.
PN WO200006737-A2.
PD 10-FEB-2000.
PA (MICR-) MICROBIAL TECHNIQS LTD.
Query Match 5.9%; Score 81.5; DB 3; Length 206;
Best Local Similarity 20.2%; Pred. No. 2.5;
RESULT 1469
ID ADR96056 standard; protein; 208 AA.
DE Novel S. pneumoniae protein sequence, SEQ ID 4691.
PN US6800744-B1.
PD 05-OCT-2004.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.9%; Score 81.5; DB 8; Length 208;
Best Local Similarity 20.2%; Pred. No. 2.5;
RESULT 1470
ID AEA59926 standard; protein; 208 AA.
DE Streptococcus pneumoniae ORF amino acid sequence SEQ ID NO:4691.
PN US2005136404-A1.
PD 23-JUN-2005.
PA (DOJC/) DOUCETTE-STAMM L A.
PA (BUSH/) BUSH D.
Query Match 5.9%; Score 81.5; DB 9; Length 208;
Best Local Similarity 20.2%; Pred. No. 2.5;
RESULT 1471
ID ABU41035 standard; protein; 278 AA.
DE Protein encoded by Prokaryotic essential gene #26562.
PN WO200277183-A2.
PD 03-OCT-2002.

PA (ELIT-) ELITRA PHARM INC.
Query Match 5.9%; Score 81.5; DB 6; Length 278;
Best Local Similarity 21.0%; Pred. No. 3.7;
RESULT 1472
ID ADF05890 standard; protein; 280 AA.
DE Bacterial polypeptide #2003.
PN US6605709-B1.
PD 12-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.9%; Score 81.5; DB 7; Length 280;
Best Local Similarity 21.0%; Pred. No. 3.7;
RESULT 1473
ID ADV10132 standard; protein; 332 AA.
DE Plant full length insert polypeptide seqid 65947.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABR/) TABASKA J E.
PA (CAOV/) CAO Y.
Query Match 5.9%; Score 81.5; DB 8; Length 332;
Best Local Similarity 21.8%; Pred. No. 4.7;
RESULT 1474
ID ABB91156 standard; protein; 351 AA.
DE Herbicidally active polypeptide SEQ ID NO 367.
PN WO200210210-A2.
PD 07-FEB-2002.
PA (FARB) BAYER AG.
Query Match 5.9%; Score 81.5; DB 5; Length 351;
Best Local Similarity 23.1%; Pred. No. 5.1;
RESULT 1475
ID AAM93355 standard; protein; 399 AA.
DE Human polypeptide, SEQ ID NO: 2909.
PN EP1130094-A2.
PD 05-SEP-2001.
PA (HELI-) HELIX RES INST.
Query Match 5.9%; Score 81.5; DB 4; Length 399;
Best Local Similarity 22.8%; Pred. No. 6.1;
RESULT 1476
ID ADL30876 standard; protein; 399 AA.
DE Human protein encoded by a full length cDNA clone SeqID 2909.
PN EP1396543-A2.
PD 10-MAR-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 5.9%; Score 81.5; DB 8; Length 399;
Best Local Similarity 22.6%; Pred. No. 6.1;
RESULT 1477
ID ABU39717 standard; protein; 425 AA.
DE Protein encoded by Prokaryotic essential gene #25244.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.9%; Score 81.5; DB 6; Length 425;
Best Local Similarity 19.6%; Pred. No. 6.6;
RESULT 1478
ID AAU33707 standard; protein; 438 AA.
DE Pseudomonas aeruginosa cellular proliferation protein #151.
PN WO200170955-A2.
PD 27-SEP-2001.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.9%; Score 81.5; DB 4; Length 438;
Best Local Similarity 20.3%; Pred. No. 6.9;
RESULT 1479
ID ABU15597 standard; protein; 438 AA.
DE Protein encoded by Prokaryotic essential gene #1124.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.9%; Score 81.5; DB 6; Length 438;
Best Local Similarity 20.3%; Pred. No. 6.9;
RESULT 1480
ID ABO83917 standard; protein; 503 AA.
DE Pseudomonas aeruginosa polypeptide #16092.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.9%; Score 81.5; DB 7; Length 503;
Best Local Similarity 20.3%; Pred. No. 8.4;
RESULT 1481
ID ABP65039 standard; protein; 234 AA.
DE Mouse membrane spanning 4-domain family, subfamily A 7 protein.
PN WO200262946-A2.
PD 15-AUG-2002.
PA (UYDU-) UNIV DUKE.
Query Match 5.8%; Score 81; DB 5; Length 234;
Best Local Similarity 20.6%; Pred. No. 3.3;
RESULT 1482
ID ADP43824 standard; protein; 293 AA.
DE Chlamydia trachomatis immunogenic protein, SEQ ID No 119.
PN WO2003049762-A2.
PD 19-JUN-2003.
PA (CHIR-) CHIRON SPA.
Query Match 5.8%; Score 81; DB 7; Length 293;
Best Local Similarity 18.4%; Pred. No. 4.5;
RESULT 1483
ID AEA19116 standard; protein; 293 AA.
DE Chlamydia trachomatis protein - SEQ ID 119.
PN US2005106162-A1.
PD 19-MAY-2005.
PA (GRAN/) GRANDI G.
PA (RATT/) RATTI G.
Query Match 5.8%; Score 81; DB 9; Length 293;
Best Local Similarity 18.4%; Pred. No. 4.5;
RESULT 1484
ID ADA34894 standard; protein; 323 AA.
DE Acinetobacter baumannii protein #2055.
PN US6562958-B1.
PD 13-MAY-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.8%; Score 81; DB 6; Length 323;
Best Local Similarity 22.5%; Pred. No. 5.2;
RESULT 1485
ID AAO20532 standard; protein; 392 AA.
DE Protein of the human TFM-2 gene sequence.
PN WO200229041-A2.
PD 11-APR-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 5.8%; Score 81; DB 5; Length 392;
Best Local Similarity 17.8%; Pred. No. 6.8;
RESULT 1486
ID AEF18843 standard; protein; 392 AA.
DE Human Transporter Family Member-2, TFM-2.
PN US2006008819-A1.
PD 12-JAN-2006.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 5.8%; Score 81; DB 10; Length 392;
Best Local Similarity 17.8%; Pred. No. 6.8;
RESULT 1487
ID ADD37455 standard; protein; 394 AA.
DE Human transporter TFM-2.
PN US2003143675-A1.
PD 31-JUL-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 5.8%; Score 81; DB 7; Length 394;
Best Local Similarity 17.8%; Pred. No. 6.8;
RESULT 1488
ID ABO61692 standard; protein; 425 AA.
DE Klebsiella pneumoniae polypeptide seqid 8209.
PN US6610836-B1.
PD 26-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.8%; Score 81; DB 7; Length 425;
Best Local Similarity 22.7%; Pred. No. 7.6;
RESULT 1489

ID AAE21184 standard; protein; 515 AA.
 DE Human TRICH-28 protein.
 PN WO200212340-A2.
 PD 14-FEB-2002.
 PA (INCY-) INCYTE GENOMICS INC.
 Query Match 5.8%; Score 81; DB 5; Length 515;
 Best Local Similarity 17.8%; Pred. No. 9.9;
 RESULT 1490
 ID ABJ37907 standard; protein; 515 AA.
 DE NOVX protein sequence SEQ ID NO 60.
 PN WO200281517-A2.
 PD 17-OCT-2002.
 PA (CURA-) CURAGEN CORP.
 Query Match 5.8%; Score 81; DB 6; Length 515;
 Best Local Similarity 17.8%; Pred. No. 9.9;
 RESULT 1491
 ID ADQ66916 standard; protein; 515 AA.
 DE Novel human protein sequence #1889.
 PN EP1440981-A2.
 PD 28-JUL-2004.
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 Query Match 5.8%; Score 81; DB 8; Length 515;
 Best Local Similarity 17.8%; Pred. No. 9.9;
 RESULT 1492
 ID ABO84581 standard; protein; 515 AA.
 DE Human cancer-associated protein HPI7-001.2.
 PN WO2004074320-A2.
 PD 02-SEP-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 5.8%; Score 81; DB 8; Length 515;
 Best Local Similarity 17.8%; Pred. No. 9.9;
 RESULT 1493
 ID ADH58563 standard; protein; 516 AA.
 DE Human Na+-independent transporter-related transporter protein.
 PN WO2003076644-A2.
 PD 18-SEP-2003.
 PA (APPL-) APPLERA CORP.
 Query Match 5.8%; Score 81; DB 7; Length 516;
 Best Local Similarity 17.8%; Pred. No. 9.9;
 RESULT 1494
 ID ADN23220 standard; protein; 544 AA.
 DE Bacterial polypeptide #5873.
 PN US2003233675-A1.
 PD 18-DEC-2003.
 PA (CAOY/) CAO Y.
 PA (HINK/) HINKLE G J.
 PA (SLAT/) SLATER S C.
 PA (CHEN/) CHEN X.
 PA (GOLD/) GOLDMAN B S.
 Query Match 5.8%; Score 81; DB 8; Length 544;
 Best Local Similarity 23.0%; Pred. No. 11;
 RESULT 1495
 ID ABB64860 standard; protein; 875 AA.
 DE Drosophila melanogaster polypeptide SEQ ID NO 21372.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 5.8%; Score 81; DB 4; Length 875;
 Best Local Similarity 20.9%; Pred. No. 20;
 RESULT 1496
 ID ABU39716 standard; protein; 1102 AA.
 DE Protein encoded by Prokaryotic essential gene #25243.
 PN WO200277183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Query Match 5.8%; Score 81; DB 6; Length 1102;
 Best Local Similarity 20.0%; Pred. No. 28;
 RESULT 1497
 ID ADY52908 standard; protein; 260 AA.
 DE Nodularia spumigena ketocarotenoid-related ketolase protein - SEQ ID 4.
 PN WO2005019461-A2.
 PD 03-MAR-2005.
 PA (SUNG-) SUNGENE GMBH & CO KGAA.

Query Match 5.8%; Score 80.5; DB 9; Length 260;
 Best Local Similarity 21.1%; Pred. No. 4.4;
 RESULT 1498
 ID ADY52974 standard; protein; 264 AA.
 DE Nodularia spumigena ketocarotenoid-related ketolase protein - SEQ ID 70.
 PN WO2005019461-A2.
 PD 03-MAR-2005.
 PA (SUNG-) SUNGENE GMBH & CO KGAA.
 Query Match 5.8%; Score 80.5; DB 9; Length 264;
 Best Local Similarity 21.1%; Pred. No. 4.5;
 RESULT 1499
 ID ABO65403 standard; protein; 298 AA.
 DE Klebsiella pneumoniae polypeptide seqid 11920.
 PN US6610836-B1.
 PD 26-AUG-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Query Match 5.8%; Score 80.5; DB 7; Length 298;
 Best Local Similarity 18.5%; Pred. No. 5.3;
 RESULT 1500
 ID ABB32477 standard; protein; 359 AA.
 DE Staphylococcus aureus polypeptide SEQ ID NO 14.
 PN WO200177365-A2.
 PD 18-OCT-2001.
 PA (PHAA) PHARMACIA & UPJOHN CO.
 Query Match 5.8%; Score 80.5; DB 5; Length 359;
 Best Local Similarity 23.4%; Pred. No. 6.8;

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OM protein - protein search, using sw model

Run on: August 28, 2006, 17:41:45 ; Search time 50 Seconds
(without alignments)
465.663 Million cell updates/sec

Title: US-10-006-867-2
Perfect score: 1392
Sequence: 1 MWFOGSLFSLPVALVWTS.....YDTAPCINNERTLLSRDI 266

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : Issued Patents_AA:*

1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*

2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*

3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*

4: /EMC_Celerra_SIDS3/ptodata/2/iaa/8_COMB.pep:*

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6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*

7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1392	100.0	266	2	US-09-991-181-23 Sequence 23, Appl
2	1392	100.0	266	2	US-09-990-444-23 Sequence 23, Appl
3	1392	100.0	266	2	US-09-997-333-23 Sequence 23, Appl
4	1392	100.0	266	2	US-09-992-598-23 Sequence 23, Appl
5	1392	100.0	266	2	US-09-989-735-23 Sequence 23, Appl
6	1392	100.0	266	3	US-09-989-726-23 Sequence 23, Appl
7	1392	100.0	266	3	US-09-997-514-23 Sequence 23, Appl
8	1392	100.0	266	3	US-09-989-728-23 Sequence 23, Appl
9	1392	100.0	266	3	US-09-997-349-23 Sequence 23, Appl
10	1392	100.0	266	3	US-09-997-653-23 Sequence 23, Appl
11	1392	100.0	266	3	US-09-989-293A-23 Sequence 23, Appl
12	1388	99.7	267	2	US-09-663-600A-190 Sequence 190, App
13	595.5	42.8	172	2	US-09-663-600A-96 Sequence 96, Appl
14	479.5	34.4	238	2	US-09-724-864-38 Sequence 38, Appl
15	358	25.7	69	2	US-09-663-600A-130 Sequence 130, App
16	358	25.7	69	2	US-09-663-600A-224 Sequence 224, App
17	118	8.5	21	2	US-08-905-223-20 Sequence 20, Appl
18	118	8.5	21	2	US-09-247-155-20 Sequence 20, Appl
19	118	8.5	21	2	US-09-663-600A-20 Sequence 20, Appl
20	118	8.5	21	2	US-09-621-976-2 Sequence 2, Appl
21	118	8.5	21	2	US-09-513-999C-2 Sequence 2, Appl
22	118	8.5	21	2	US-09-471-276-2 Sequence 2, Appl
23	118	8.5	21	2	US-09-903-190-20 Sequence 20, Appl
24	91.5	6.6	291	2	US-09-107-532A-4147 Sequence 4147, Ap
25	91.5	6.6	387	2	US-09-721-870-14 Sequence 14, Appl
26	90	6.5	283	2	US-09-602-787A-588 Sequence 588, App

27	90	6.5	396	2	US-09-248-796A-20434 Sequence 20434, A
28	88	6.4	1203	2	US-10-094-749-2651 Sequence 2651, Ap
29	88	6.3	344	2	US-09-248-796A-16383 Sequence 16383, A
30	88	6.3	1165	1	US-08-240-357-2 Sequence 2, Appl
31	86.5	6.2	356	2	US-09-134-000C-4914 Sequence 4914, Ap
32	85.5	6.1	579	2	US-09-786-681A-4 Sequence 4, Appl
33	85.5	6.1	582	2	US-09-786-681A-2 Sequence 2, Appl
34	85	6.1	419	2	US-09-948-774-2 Sequence 12, Appl
35	85	6.1	1180	2	US-08-726-214-12 Sequence 12, Appl
36	84.5	6.1	296	2	US-09-134-000C-6205 Sequence 6205, Ap
37	84.5	6.1	356	2	US-10-144-929-114 Sequence 114, App
38	84.5	6.1	453	2	US-09-991-181-73 Sequence 73, Appl
39	84.5	6.1	453	2	US-09-990-444-73 Sequence 73, Appl
40	84.5	6.1	453	2	US-09-997-333-73 Sequence 73, Appl
41	84.5	6.1	453	2	US-09-992-598-73 Sequence 73, Appl
42	84.5	6.1	453	3	US-09-989-735-73 Sequence 73, Appl
43	84.5	6.1	453	3	US-09-989-726-73 Sequence 73, Appl
44	84.5	6.1	453	3	US-09-997-514-73 Sequence 73, Appl
45	84.5	6.1	453	3	US-09-989-728-73 Sequence 73, Appl
46	84.5	6.1	453	3	US-09-997-349-73 Sequence 73, Appl
47	84.5	6.1	453	3	US-09-997-653-73 Sequence 73, Appl
48	84.5	6.1	453	3	US-09-989-293A-73 Sequence 73, Appl
49	84	6.0	241	2	US-09-328-352-8001 Sequence 8001, Ap
50	84	6.0	506	2	US-09-540-236-2605 Sequence 2605, Ap
51	84	6.0	537	2	US-09-489-039A-14149 Sequence 14149, A
52	84	6.0	602	2	US-09-252-991A-22527 Sequence 22527, A
53	84	6.0	720	2	US-09-252-991A-19581 Sequence 19581, A
54	84	6.0	1138	2	US-09-489-039A-13574 Sequence 13574, A
55	83.5	6.0	618	1	US-08-332-312-2 Sequence 2, Appl
56	83	6.0	318	2	US-09-583-110-2976 Sequence 2976, Ap
57	83	6.0	336	2	US-09-107-433-5076 Sequence 5076, Ap
58	83	6.0	417	2	US-09-489-039A-8730 Sequence 8730, Ap
59	83	6.0	542	2	US-09-252-991A-19270 Sequence 19270, A
60	83	6.0	632	2	US-09-328-352-4785 Sequence 4785, Ap
61	82.5	5.9	492	2	US-08-252-991A-18139 Sequence 18139, A
62	82	5.9	299	2	US-09-393-634-5 Sequence 5, Appl
63	82	5.9	299	3	US-10-770-127-81 Sequence 81, Appl
64	82	5.9	474	2	US-09-252-991A-30354 Sequence 30354, A
65	82	5.9	574	2	US-09-248-796A-20154 Sequence 20154, A
66	82	5.9	664	2	US-09-248-796A-17191 Sequence 17191, A
67	82	5.9	1094	2	US-09-949-016-8755 Sequence 8755, Ap
68	82	5.9	1094	2	US-09-949-016-8756 Sequence 8756, Ap
69	82	5.9	1147	2	US-09-949-016-8861 Sequence 8861, Ap
70	82	5.9	1147	2	US-09-949-016-8862 Sequence 8862, Ap
71	82	5.9	1168	2	US-09-474-076-2 Sequence 2, Appl
72	82	5.9	1168	2	US-09-472-667-11 Sequence 11, Appl
73	82	5.9	1168	2	US-10-201-000-2 Sequence 2, Appl
74	81.5	5.9	199	2	US-09-583-110-3127 Sequence 3127, Ap
75	81.5	5.9	205	2	US-09-769-787-46 Sequence 46, Appl
76	81.5	5.9	208	2	US-09-107-433-4691 Sequence 4691, Ap
77	81.5	5.9	280	2	US-09-543-681A-6175 Sequence 6175, Ap
78	81.5	5.9	503	2	US-09-252-991A-32663 Sequence 32663, A
79	81	5.8	323	2	US-09-328-352-6181 Sequence 6181, Ap
80	81	5.8	394	2	US-10-154-419-28 Sequence 28, Appl
81	81	5.8	425	2	US-09-489-039A-8209 Sequence 8209, Ap
82	80.5	5.8	298	2	US-09-489-039A-11920 Sequence 11920, A
83	80.5	5.8	359	2	US-09-828-523A-14 Sequence 14, Appl
84	80.5	5.8	370	2	US-09-828-523A-74 Sequence 74, Appl
85	80.5	5.8	411	1	US-09-134-001C-3299 Sequence 3299, Ap
86	80.5	5.8	607	1	US-07-879-617A-12 Sequence 12, Appl
87	80.5	5.8	607	1	US-08-753-985-12 Sequence 12, Appl
88	80.5	5.8	834	1	US-08-677-734A-9 Sequence 9, Appl
89	80.5	5.8	834	1	US-08-677-734A-10 Sequence 10, Appl
90	80.5	5.8	834	2	US-09-097-053-9 Sequence 9, Appl
91	80.5	5.8	834	2	US-09-097-053-10 Sequence 10, Appl
92	80	5.7	221	2	US-10-094-749-2202 Sequence 2202, Ap
93	80	5.7	292	2	US-09-583-110-4530 Sequence 4530, Ap
94	80	5.7	307	2	US-09-303-518D-406 Sequence 406, App
95	80	5.7	308	2	US-09-107-433-3470 Sequence 3470, A
96	80	5.7	325	2	US-09-252-991A-18010 Sequence 18010, A
97	80	5.7	557	2	US-09-712-768-2 Sequence 2, Appl
98	79.5	5.7	271	2	US-09-328-352-7159 Sequence 7159, Ap
99	79.5	5.7	274	2	US-09-902-540-14253 Sequence 14253, A

100	79.5	5.7	308	2	US-09-328-352-7092	Sequence 7092, Ap	173	74.5	5.4	384	2	US-09-248-796A-20119	Sequence 20119, A
101	79.5	5.7	315	2	US-09-328-352-4864	Sequence 4864, Ap	174	74.5	5.4	388	2	US-09-949-016-7631	Sequence 7631, Ap
102	79.5	5.7	315	2	US-09-248-796A-15178	Sequence 15178, A	175	74.5	5.4	405	2	US-09-719-088B-3	Sequence 3, Appli
103	79.5	5.7	483	2	US-09-489-039A-7429	Sequence 7429, Ap	176	74.5	5.4	407	2	US-09-364-425B-23	Sequence 23, Appli
104	79.5	5.7	831	1	US-08-677-734A-11	Sequence 11, Appl	177	74.5	5.4	436	7	5432081-10	Patent No. 5432081
105	79.5	5.7	831	2	US-09-097-053-11	Sequence 11, Appl	178	74.5	5.4	443	2	US-09-328-352-7069	Sequence 7069, Ap
106	79	5.7	298	2	US-09-438-185A-545	Sequence 545, App	179	74.5	5.4	475	2	US-09-248-796A-20067	Sequence 20067, A
107	79	5.7	307	2	US-09-303-518D-404	Sequence 404, App	180	74.5	5.4	556	2	US-09-248-796A-20229	Sequence 20229, A
108	79	5.7	491	2	US-09-543-681A-1195	Sequence 4195, Ap	181	74.5	5.4	601	1	US-08-194-338-2	Sequence 2, Appli
109	79	5.7	600	2	US-09-134-000C-5694	Sequence 5694, Ap	182	74.5	5.4	824	2	US-09-605-703B-358	Sequence 358, App
110	79	5.7	670	2	US-09-489-039A-7251	Sequence 7251, Ap	183	74.5	5.4	832	2	US-09-605-703B-356	Sequence 356, App
111	78.5	5.6	320	4	US-10-038-895A-5	Sequence 5, Appli	184	74.5	5.4	1798	2	US-09-270-767-60233	Sequence 60233, A
112	78.5	5.6	473	2	US-09-543-681A-7980	Sequence 7980, Ap	185	74.5	5.4	2410	2	US-09-270-767-44775	Sequence 44775, A
113	78.5	5.6	793	2	US-09-900-237-18	Sequence 18, Appl	186	74	5.3	173	2	US-09-252-991A-22033	Sequence 22033, A
114	78.5	5.6	832	1	US-08-677-734A-12	Sequence 12, Appl	187	74	5.3	262	2	US-09-328-352-6026	Sequence 6026, Ap
115	78.5	5.6	832	2	US-09-097-053-12	Sequence 12, Appl	188	74	5.3	280	2	US-09-328-352-889	Sequence 889, App
116	78	5.6	221	2	US-09-248-796A-16814	Sequence 16814, A	189	74	5.3	280	2	US-09-438-185A-829	Sequence 829, App
117	78	5.6	292	2	US-09-540-236-3287	Sequence 3287, Ap	190	74	5.3	282	2	US-09-583-110-3219	Sequence 3219, Ap
118	78	5.6	405	2	US-09-144-914-5	Sequence 5, Appli	191	74	5.3	292	1	US-09-024-848-2	Sequence 2, Appli
119	78	5.6	575	2	US-09-328-352-6465	Sequence 6465, Ap	192	74	5.3	292	2	US-09-348-116A-2	Sequence 2, Appli
120	78	5.6	664	2	US-09-502-540-16458	Sequence 16458, A	193	74	5.3	307	2	US-09-303-518D-408	Sequence 408, App
121	77.5	5.6	238	2	US-09-328-352-7122	Sequence 7122, Ap	194	74	5.3	332	2	US-09-902-540-15291	Sequence 15291, A
122	77.5	5.6	287	2	US-09-543-681A-5282	Sequence 5282, Ap	195	74	5.3	407	2	US-09-303-518D-802	Sequence 802, App
123	77.5	5.6	525	2	US-09-252-991A-27543	Sequence 27543, A	196	74	5.3	445	2	US-08-937-834-5	Sequence 5, Appli
124	77.5	5.6	693	2	US-10-094-749-2517	Sequence 2517, Ap	197	74	5.3	448	2	US-09-543-681A-7245	Sequence 7245, Ap
125	77.5	5.6	743	2	US-10-104-047-2340	Sequence 2340, Ap	198	74	5.3	487	2	US-09-949-016-9649	Sequence 9649, Ap
126	77.5	5.6	1162	2	US-09-252-991A-32764	Sequence 32764, A	199	74	5.3	800	2	US-09-543-681A-7968	Sequence 7968, Ap
127	77	5.5	318	2	US-09-710-279-3118	Sequence 3118, Ap	200	74	5.3	937	2	US-09-949-002-536	Sequence 536, App
128	77	5.5	385	2	US-09-540-236-3736	Sequence 3736, Ap	201	74	5.3	937	2	US-09-489-039A-8466	Sequence 8466, Ap
129	77	5.5	506	2	US-09-719-919A-1	Sequence 1, Appli	202	73.5	5.3	360	1	US-08-597-236-11	Sequence 11, Appl
130	77	5.5	532	2	US-09-107-532A-7299	Sequence 7299, Ap	203	73.5	5.3	360	1	US-08-746-682A-11	Sequence 11, Appl
131	76.5	5.5	397	2	US-09-328-352-7457	Sequence 7457, Ap	204	73.5	5.3	391	1	US-07-921-178A-2	Sequence 2, Appli
132	76.5	5.5	483	2	US-09-710-279-3132	Sequence 3132, Ap	205	73.5	5.3	391	1	US-08-103-445-5	Sequence 5, Appli
133	76.5	5.5	596	2	US-09-949-016-6719	Sequence 6719, Ap	206	73.5	5.3	391	1	US-08-461-650B-5	Sequence 5, Appli
134	76.5	5.5	630	2	US-09-134-001C-4615	Sequence 4615, Ap	207	73.5	5.3	391	1	US-08-501-003A-16	Sequence 16, Appl
135	76.5	5.5	729	2	US-10-094-749-2118	Sequence 2118, Ap	208	73.5	5.3	391	2	US-09-543-681A-8292	Sequence 8292, Ap
136	76.5	5.5	320	2	US-09-543-681A-7972	Sequence 7972, Ap	209	73.5	5.3	391	2	US-09-275-252A-13	Sequence 13, Appl
137	76	5.5	322	2	US-09-134-001C-4064	Sequence 4064, Ap	210	73.5	5.3	395	2	US-09-489-039A-12123	Sequence 12123, A
138	76	5.5	361	2	US-09-482-273-236	Sequence 236, App	211	73.5	5.3	395	2	US-09-543-681A-5455	Sequence 5455, Ap
139	76	5.5	424	2	US-09-107-532A-6500	Sequence 6500, Ap	212	73.5	5.3	416	2	US-09-107-532A-4001	Sequence 4001, Ap
140	76	5.5	438	2	US-09-252-991A-18895	Sequence 18895, A	213	73.5	5.3	417	2	US-09-198-452A-720	Sequence 720, App
141	76	5.5	424	2	US-09-922-501-10	Patent No. 5268463	214	73.5	5.3	428	2	US-09-438-185A-682	Sequence 682, App
142	76	5.5	435	7	5268463-9	Sequence 10, Appl	215	73.5	5.3	514	2	US-09-489-039A-11902	Sequence 11902, A
143	76	5.5	435	7	5268463-9	Sequence 10, Appl	216	73.5	5.3	564	2	US-09-902-540-16018	Sequence 16018, A
144	76	5.5	453	2	US-09-252-991A-17394	Sequence 17394, A	217	73.5	5.3	607	1	US-07-959-943-7	Sequence 7, Appli
145	76	5.5	633	2	US-09-949-016-10337	Sequence 10337, A	218	73.5	5.3	630	1	US-07-959-943-9	Sequence 9, Appli
146	75.5	5.4	313	2	US-09-252-991A-27163	Sequence 27163, A	219	73.5	5.3	693	2	US-09-252-991A-19167	Sequence 19167, A
147	75.5	5.4	401	2	US-09-489-039A-11546	Sequence 11546, A	220	73.5	5.3	717	2	US-09-134-000C-5833	Sequence 5833, Ap
148	75.5	5.4	445	2	US-09-328-352-6669	Sequence 6669, Ap	221	73.5	5.3	1099	2	US-08-726-214-14	Sequence 14, Appl
149	75.5	5.4	517	2	US-09-248-796A-20437	Sequence 20437, A	222	73.5	5.3	1099	2	US-07-551-531-2	Sequence 2, Appli
150	75.5	5.4	717	2	US-09-854-122-49	Sequence 49, Appl	223	73.5	5.3	2485	5	PCT-US94-00198-1	Sequence 1, Appli
151	75.5	5.4	1155	2	US-09-543-681A-6286	Sequence 6286, Ap	224	73.5	5.3	2485	5	PCT-US94-00198-2	Sequence 2, Appli
152	75.5	5.4	1172	2	US-09-328-352-6071	Sequence 6071, Ap	225	73.5	5.3	2485	5	PCT-US94-00198-2	Sequence 2, Appli
153	75	5.4	218	2	US-09-328-352-5215	Sequence 5215, Ap	226	73.5	5.3	2818	1	US-08-510-284-1	Sequence 1, Appli
154	75	5.4	283	2	US-09-107-433-3024	Sequence 3024, Ap	227	73.5	5.3	2818	1	US-08-411-389-2	Sequence 2, Appli
155	75	5.4	290	2	US-09-134-001C-4893	Sequence 4893, Ap	228	73.5	5.3	2818	1	US-08-449-933-2	Sequence 2, Appli
156	75	5.4	344	1	US-08-689-974-1	Sequence 1, Appli	229	73.5	5.3	2818	2	US-07-966-049A-2	Sequence 2, Appli
157	75	5.4	344	2	US-09-058-376-1	Sequence 1, Appli	230	73.5	5.3	2818	2	US-09-542-331-2	Sequence 2, Appli
158	75	5.4	394	2	US-09-144-914-4	Sequence 4, Appli	231	73.5	5.3	2818	2	US-09-510-791-2	Sequence 2, Appli
159	75	5.4	394	2	US-09-655-272-5	Sequence 5, Appli	232	73	5.2	187	2	US-09-328-352-5593	Sequence 5593, Ap
160	75	5.4	399	2	US-09-489-039A-9414	Sequence 9414, Ap	233	73	5.2	187	2	US-09-328-352-7918	Sequence 7918, Ap
161	75	5.4	408	2	US-09-719-088B-2	Sequence 2, Appli	234	73	5.2	234	2	US-09-270-767-45527	Sequence 45527, A
162	75	5.4	420	2	US-09-255-368-6	Sequence 6, Appli	235	73	5.2	291	2	US-09-252-991A-32938	Sequence 32938, A
163	75	5.4	420	2	US-08-405-558-6	Sequence 6, Appli	236	73	5.2	431	2	US-09-710-279-2566	Sequence 2566, Ap
164	75	5.4	420	2	US-09-538-036-6	Sequence 6, Appli	237	73	5.2	434	2	US-09-328-352-7304	Sequence 7304, Ap
165	75	5.4	457	2	US-09-489-039A-8037	Sequence 8037, Ap	238	73	5.2	445	1	US-08-900-148-2	Sequence 2, Appli
166	75	5.4	524	2	US-09-248-796A-20256	Sequence 20256, A	239	73	5.2	466	2	US-09-134-001C-3355	Sequence 3355, Ap
167	75	5.4	579	2	US-09-720-317A-4	Sequence 4, Appli	240	73	5.2	727	2	US-09-815-923-10	Sequence 10, Appl
168	74.5	5.4	304	2	US-09-328-352-6459	Sequence 6459, Ap	241	73	5.2	3079	5	PCT-US94-00198-4	Sequence 4, Appli
169	74.5	5.4	321	2	US-09-252-991A-31084	Sequence 31084, A	242	72.5	5.2	227	2	US-09-583-110-3621	Sequence 3621, Ap
170	74.5	5.4	340	2	US-09-543-681A-5778	Sequence 5778, Ap	243	72.5	5.2	281	2	US-09-540-236-2349	Sequence 2349, Ap
171	74.5	5.4	367	2	US-09-198-452A-1069	Sequence 1069, Ap	244	72.5	5.2	319	2	US-09-543-681A-5398	Sequence 5398, Ap
172	74.5	5.4	367	2	US-09-438-185A-996	Sequence 996, App	245	72.5	5.2	389	2	US-09-328-352-5055	Sequence 5055, Ap

246	72.5	5.2	413	2	US-09-540-236-3672	Sequence 3672, Ap	319	71	5.1	384	2	US-09-902-540-11956	Sequence 11956, A
247	72.5	5.2	519	2	US-09-489-039A-13346	Sequence 13346, A	320	71	5.1	388	2	US-09-222-938A-37	Sequence 37, Appl
248	72.5	5.2	519	2	US-09-248-796A-20368	Sequence 20368, A	331	71	5.1	397	2	US-09-583-110-2946	Sequence 2946, Ap
249	72.5	5.2	607	2	US-09-328-352-5096	Sequence 5096, Ap	332	71	5.1	404	2	US-09-107-433-3747	Sequence 3747, Ap
250	72	5.2	261	2	US-09-538-092-318	Sequence 318, App	333	71	5.1	408	2	US-09-489-039A-9583	Sequence 9583, Ap
251	72	5.2	273	2	US-09-328-352-5843	Sequence 5843, Ap	334	71	5.1	454	2	US-09-489-847-305	Sequence 305, App
252	72	5.2	337	2	US-09-902-540-13005	Sequence 13005, A	335	71	5.1	461	2	US-09-043-944-1	Sequence 1, Appl
253	72	5.2	347	2	US-09-303-518D-804	Sequence 804, App	336	71	5.1	461	2	US-09-043-944-6	Sequence 6, Appl
254	72	5.2	355	2	US-09-170-496D-2	Sequence 2, Appl	337	71	5.1	461	2	US-10-811-199-1	Sequence 1, Appl
255	72	5.2	430	2	US-09-134-001C-2981	Sequence 2981, Ap	338	71	5.1	461	2	US-10-811-199-6	Sequence 6, Appl
256	72	5.2	468	2	US-09-543-681A-4671	Sequence 4671, Ap	339	71	5.1	465	2	US-09-710-279-1676	Sequence 1676, Ap
257	72	5.2	495	2	US-09-359-167-4	Sequence 4, Appl	340	71	5.1	466	2	US-09-328-352-7117	Sequence 7117, Ap
258	72	5.2	502	2	US-09-579-250-12	Sequence 12, Appl	341	71	5.1	502	1	US-08-278-635B-7	Sequence 7, Appl
259	72	5.2	502	2	US-09-579-250-14	Sequence 14, Appl	342	71	5.1	502	1	US-08-466-589-8	Sequence 8, Appl
260	72	5.2	506	2	US-09-252-991A-25852	Sequence 25852, A	343	71	5.1	502	1	US-08-700-636-8	Sequence 8, Appl
261	72	5.2	569	1	US-08-750-723A-2	Sequence 2, Appl	344	71	5.1	502	1	US-08-464-258B-7	Sequence 7, Appl
262	72	5.2	569	2	US-09-191-275-2	Sequence 2, Appl	345	71	5.1	502	2	US-08-467-574-8	Sequence 8, Appl
263	72	5.2	906	1	US-08-190-802A-31	Sequence 31, Appl	346	71	5.1	502	2	US-08-471-961-7	Sequence 7, Appl
264	72	5.2	906	2	US-08-477-346-31	Sequence 31, Appl	347	71	5.1	502	2	US-09-217-345-8	Sequence 8, Appl
265	72	5.2	906	2	US-08-473-089-31	Sequence 31, Appl	348	71	5.1	502	2	US-08-487-596-12	Sequence 12, Appl
266	72	5.2	906	2	US-08-487-072A-31	Sequence 31, Appl	349	71	5.1	502	2	US-09-345-109C-7	Sequence 7, Appl
267	71.5	5.1	228	2	US-09-973-278-160	Sequence 160, App	350	71	5.1	502	2	US-09-892-985-8	Sequence 8, Appl
268	71.5	5.1	229	2	US-09-227-357-237	Sequence 237, App	351	71	5.1	502	2	US-09-579-250-2	Sequence 2, Appl
269	71.5	5.1	237	1	US-08-818-514-3	Sequence 3, Appl	352	71	5.1	502	2	US-09-579-250-10	Sequence 10, Appl
270	71.5	5.1	237	2	US-09-115-934A-3	Sequence 3, Appl	353	71	5.1	502	2	US-09-703-951A-12	Sequence 12, Appl
271	71.5	5.1	237	2	US-09-611-175-3	Sequence 3, Appl	354	71	5.1	502	2	US-09-252-991A-28549	Sequence 28549, A
272	71.5	5.1	277	2	US-09-303-518D-402	Sequence 402, App	355	71	5.1	594	2	US-09-650-324A-59	Sequence 59, Appl
273	71.5	5.1	287	2	US-09-134-001C-5055	Sequence 5055, Ap	356	71	5.1	594	2	US-10-039-112A-59	Sequence 59, Appl
274	71.5	5.1	292	2	US-09-489-039A-12212	Sequence 12212, A	357	71	5.1	627	2	US-09-902-540-15743	Sequence 15743, A
275	71.5	5.1	309	3	US-10-770-127-22	Sequence 22, Appl	358	71	5.1	658	1	US-08-825-558-4	Sequence 4, Appl
276	71.5	5.1	372	1	US-08-501-003A-12	Sequence 12, Appl	359	71	5.1	658	2	US-09-312-611-4	Sequence 4, Appl
277	71.5	5.1	379	2	US-09-740-035-4	Sequence 4, Appl	360	71	5.1	693	2	US-09-999-833A-483	Sequence 483, App
278	71.5	5.1	379	2	US-10-056-790-8	Sequence 8, Appl	361	71	5.1	693	2	US-10-020-445A-483	Sequence 483, App
279	71.5	5.1	379	2	US-10-056-790-40	Sequence 40, Appl	362	71	5.1	693	2	US-09-978-189-483	Sequence 483, App
280	71.5	5.1	383	1	US-08-501-003A-14	Sequence 14, Appl	363	71	5.1	693	2	US-10-017-085A-483	Sequence 483, App
281	71.5	5.1	389	1	US-08-501-003A-11	Sequence 11, Appl	364	71	5.1	693	3	US-10-145-129A-483	Sequence 483, App
282	71.5	5.1	391	1	US-08-501-003A-13	Sequence 13, Appl	365	71	5.1	693	3	US-10-013-929A-483	Sequence 483, App
283	71.5	5.1	391	2	US-09-949-016-590A	Sequence 590A, Ap	366	71	5.1	693	3	US-10-013-917A-483	Sequence 7, Appl
284	71.5	5.1	398	1	US-08-501-003A-15	Sequence 15, Appl	367	71	5.1	859	2	US-09-313-942-7	Sequence 7, Appl
285	71.5	5.1	411	2	US-09-949-016-8100	Sequence 8100, Ap	368	71	5.1	859	2	US-10-282-162-6	Sequence 6, Appl
286	71.5	5.1	412	2	US-10-138-701-59	Sequence 59, Appl	369	71	5.1	918	1	US-08-825-558-6	Sequence 6, Appl
287	71.5	5.1	484	2	US-09-248-796A-20357	Sequence 20357, A	370	71	5.1	918	2	US-09-312-611-6	Sequence 6, Appl
288	71.5	5.1	519	2	US-09-198-452A-561	Sequence 561, App	371	71	5.1	918	2	US-09-853-180B-3	Sequence 3, Appl
289	71.5	5.1	521	2	US-09-438-185A-523	Sequence 523, App	372	71	5.1	918	2	US-09-949-002-333	Sequence 333, App
290	71.5	5.1	535	2	US-09-252-991A-21652	Sequence 21652, A	373	71	5.1	922	2	US-09-569-611C-41	Sequence 41, Appl
291	71.5	5.1	552	2	US-09-270-767-45540	Sequence 45540, A	374	71	5.1	951	2	US-09-313-942-9	Sequence 9, Appl
292	71.5	5.1	574	2	US-09-248-796A-20132	Sequence 20132, A	375	71	5.1	951	2	US-10-282-162-9	Sequence 9, Appl
293	71.5	5.1	587	2	US-08-635-552A-3	Sequence 3, Appl	376	71	5.1	971	2	US-09-868-572A-1	Sequence 1, Appl
294	71	5.1	201	2	US-09-270-767-33463	Sequence 33463, A	377	70.5	5.1	150	2	US-09-134-000C-4337	Sequence 4337, Ap
295	71	5.1	201	2	US-09-270-767-48680	Sequence 48680, A	378	70.5	5.1	286	2	US-09-248-796A-17897	Sequence 17897, A
296	71	5.1	261	2	US-10-012-231A-326	Sequence 326, App	379	70.5	5.1	319	2	US-09-130-749-2	Sequence 2, Appl
297	71	5.1	261	2	US-10-015-389A-326	Sequence 326, App	380	70.5	5.1	319	2	US-09-130-749-2	Sequence 2, Appl
298	71	5.1	261	2	US-10-006-768A-326	Sequence 326, App	381	70.5	5.1	319	2	US-09-170-496D-60	Sequence 60, Appl
299	71	5.1	261	2	US-10-015-671A-326	Sequence 326, App	382	70.5	5.1	319	2	US-09-949-016-10000	Sequence 10000, A
300	71	5.1	261	2	US-10-015-393A-326	Sequence 326, App	383	70.5	5.1	386	2	US-09-489-039A-12240	Sequence 12240, A
301	71	5.1	261	2	US-10-011-833A-326	Sequence 326, App	384	70.5	5.1	387	2	US-09-543-681A-6203	Sequence 6203, Ap
302	71	5.1	261	2	US-10-006-041A-326	Sequence 326, App	385	70.5	5.1	395	2	US-09-489-039A-8272	Sequence 8272, Ap
303	71	5.1	261	2	US-10-012-064A-326	Sequence 326, App	386	70.5	5.1	399	2	US-09-134-001C-8272	Sequence 3805, Ap
304	71	5.1	261	2	US-10-015-392A-326	Sequence 326, App	387	70.5	5.1	420	2	US-09-489-039A-8166	Sequence 8166, Ap
305	71	5.1	261	3	US-10-011-795B-326	Sequence 326, App	388	70.5	5.1	443	2	US-09-328-352-5249	Sequence 5249, Ap
306	71	5.1	261	3	US-10-015-386A-326	Sequence 326, App	389	70.5	5.1	444	2	US-08-748-485-1	Sequence 1, Appl
307	71	5.1	261	3	US-10-012-121A-326	Sequence 326, App	390	70.5	5.1	454	1	US-09-107-532A-6175	Sequence 6175, Ap
308	71	5.1	261	3	US-10-006-485A-326	Sequence 326, App	391	70.5	5.1	467	2	US-09-934-899-10	Sequence 10, Appl
309	71	5.1	261	3	US-10-006-746A-326	Sequence 326, App	392	70.5	5.1	472	2	US-09-934-868-30	Sequence 30, Appl
310	71	5.1	261	3	US-10-012-752A-326	Sequence 326, App	393	70.5	5.1	472	2	US-10-701-200-30	Sequence 30, Appl
311	71	5.1	261	3	US-10-017-253A-326	Sequence 326, App	394	70.5	5.1	473	2	US-09-949-016-11735	Sequence 11735, A
312	71	5.1	261	3	US-10-015-519A-326	Sequence 326, App	395	70.5	5.1	474	2	US-09-486-192-4	Sequence 4, Appl
313	71	5.1	261	3	US-10-015-715A-326	Sequence 326, App	396	70.5	5.1	474	2	US-10-328-459A-4	Sequence 4, Appl
314	71	5.1	261	3	US-10-007-236A-326	Sequence 326, App	397	70.5	5.1	500	2	US-09-489-039A-10995	Sequence 10995, A
315	71	5.1	332	2	US-09-313-942-10	Sequence 10, Appl	398	70.5	5.1	619	2	US-09-248-796A-20837	Sequence 20837, A
316	71	5.1	332	2	US-10-282-162-10	Sequence 10, Appl	399	70.5	5.1	669	2	US-09-949-016-6720	Sequence 6720, Ap
317	71	5.1	347	2	US-09-769-787-20	Sequence 20, Appl	390	70.5	5.1	681	2	US-09-248-796A-20121	Sequence 20121, A
318	71	5.1	369	2	US-09-838-955A-3	Sequence 3, Appl	391	70.5	5.1	687	3	US-10-179-410-2	Sequence 2, Appl

392	70.5	5.1	877	1	US-08-072-574-12	Sequence 12, Appl	465	69	5.0	308	2	US-09-438-185A-569	Sequence 569, App
393	70.5	5.1	955	2	US-09-252-991A-18882	Sequence 18882, A	466	69	5.0	309	2	US-10-111-105B-2	Sequence 2, Appl
394	70.5	5.1	1134	2	US-08-726-213-2	Sequence 2, Appl	467	69	5.0	316	1	US-08-827-291A-2	Sequence 2, Appl
395	70.5	5.1	1134	2	US-09-245-039-2	Sequence 2, Appl	468	69	5.0	321	2	US-10-314-048A-10	Sequence 10, Appl
396	70.5	5.1	1681	1	US-09-920-653B-3	Sequence 3, Appl	469	69	5.0	344	2	US-10-121-757B-20	Sequence 20, Appl
397	70.5	5.1	1788	1	US-08-962-284-2	Sequence 2, Appl	470	69	5.0	359	2	US-09-875-076-28	Sequence 28, Appl
398	70	5.0	139	2	US-09-489-039A-8585	Sequence 8585, Ap	471	69	5.0	380	1	US-08-237-108-16	Sequence 16, Appl
399	70	5.0	235	2	US-09-252-991A-19945	Sequence 19945, A	472	69	5.0	380	1	US-09-073-674-16	Sequence 16, Appl
400	70	5.0	296	2	US-09-328-352-7482	Sequence 7482, Ap	473	69	5.0	397	2	US-09-328-352-7357	Sequence 7357, Ap
401	70	5.0	314	2	US-09-543-681A-6497	Sequence 6497, Ap	474	69	5.0	403	2	US-09-328-352-5907	Sequence 5907, Ap
402	70	5.0	429	2	US-09-156-809-1	Sequence 1, Appl	475	69	5.0	420	2	US-09-248-796A-20349	Sequence 20349, A
403	70	5.0	429	2	US-10-006-915-1	Sequence 1, Appl	476	69	5.0	446	2	US-09-303-518D-150	Sequence 150, App
404	70	5.0	496	2	US-09-328-352-6875	Sequence 6875, Ap	477	69	5.0	451	2	US-09-303-518D-152	Sequence 152, App
405	70	5.0	502	2	US-09-489-039A-8772	Sequence 8772, Ap	478	69	5.0	451	2	US-09-073-674-16	Sequence 2, Appl
406	70	5.0	502	2	US-08-771-737-2	Sequence 2, Appl	479	69	5.0	466	2	US-09-762-278-2	Sequence 2, Appl
407	70	5.0	502	2	US-09-954-936-2	Sequence 2, Appl	480	69	5.0	483	2	US-09-134-000C-4234	Sequence 4234, Ap
408	70	5.0	526	2	US-09-543-681A-6494	Sequence 6494, Ap	481	69	5.0	506	2	US-09-540-236-2360	Sequence 2360, Ap
409	70	5.0	535	2	US-09-252-991A-21805	Sequence 21805, A	482	69	5.0	520	2	US-09-248-796A-20803	Sequence 20803, A
410	70	5.0	539	2	US-09-538-092-741	Sequence 741, App	483	69	5.0	583	2	US-09-489-039A-13918	Sequence 13918, A
411	70	5.0	560	2	US-09-999-833A-420	Sequence 420, App	484	69	5.0	642	2	US-09-252-991A-23588	Sequence 23588, A
412	70	5.0	560	2	US-10-020-445A-420	Sequence 420, App	485	69	5.0	719	2	US-09-328-352-6274	Sequence 6274, Ap
413	70	5.0	560	2	US-09-978-189-420	Sequence 420, App	486	69	5.0	852	2	US-09-254-344-4	Sequence 4, Appl
414	70	5.0	560	2	US-10-017-085A-420	Sequence 420, App	487	69	5.0	854	2	US-09-254-352B-18	Sequence 18, Appl
415	70	5.0	560	3	US-10-145-129A-420	Sequence 420, App	488	69	5.0	934	1	US-08-215-805A-80	Sequence 80, Appl
416	70	5.0	560	3	US-10-013-929A-420	Sequence 420, App	489	69	5.0	1095	2	US-09-112-096-15	Sequence 15, Appl
417	70	5.0	560	3	US-10-013-917A-420	Sequence 420, App	490	69	5.0	1095	2	US-09-636-215-778	Sequence 778, App
418	70	5.0	594	2	US-09-489-039A-10622	Sequence 10622, A	491	69	5.0	1095	2	US-09-685-166A-778	Sequence 778, App
419	70	5.0	688	2	US-09-438-185A-870	Sequence 870, App	492	69	5.0	1095	2	US-09-679-426-778	Sequence 778, App
420	70	5.0	708	1	US-07-797-556-2	Sequence 2, Appl	493	69	5.0	1095	2	US-09-759-143-778	Sequence 778, App
421	70	5.0	708	1	US-08-308-881-2	Sequence 2, Appl	494	69	5.0	1095	2	US-09-651-236-778	Sequence 778, App
422	70	5.0	708	1	US-09-058-263-2	Sequence 2, Appl	495	69	5.0	1095	2	US-09-657-279-778	Sequence 778, App
423	70	5.0	708	1	US-09-059-099-2	Sequence 2, Appl	496	69	5.0	1095	2	US-10-012-896-778	Sequence 778, App
424	70	5.0	708	2	US-09-058-264-2	Sequence 2, Appl	497	69	5.0	1095	3	US-10-144-678A-778	Sequence 778, App
425	70	5.0	708	2	US-09-455-962-2	Sequence 2, Appl	498	69	5.0	1180	1	US-08-072-574-8	Sequence 8, Appl
426	70	5.0	708	5	PCT-US95-06530-2	Sequence 2, Appl	499	69	5.0	1212	1	US-08-072-574-10	Sequence 10, Appl
427	70	5.0	1028	2	US-09-328-352-5749	Sequence 5749, Ap	500	69	5.0	2037	2	US-09-543-681A-5538	Sequence 5538, Ap
428	70	5.0	1165	2	US-09-949-016-6874	Sequence 6874, Ap	501	69	5.0	2873	1	US-08-466-033-15	Sequence 15, Appl
429	70	5.0	1165	1	US-09-949-016-11392	Sequence 11392, A	502	69	5.0	2873	1	US-08-638-911A-2	Sequence 2, Appl
430	70	5.0	2105	1	US-08-808-793-3	Sequence 3, Appl	503	69	5.0	2873	1	US-08-444-733-15	Sequence 15, Appl
431	70	5.0	2105	2	US-08-772-512A-3	Sequence 3, Appl	504	69	5.0	2873	1	US-08-464-134-15	Sequence 15, Appl
432	70	5.0	2105	2	US-09-428-371-3	Sequence 3, Appl	505	69	5.0	2873	1	US-08-461-361-15	Sequence 15, Appl
433	69.5	5.0	2105	2	US-09-902-540-11200	Sequence 11200, A	506	69	5.0	2873	1	US-08-485-910-15	Sequence 15, Appl
434	69.5	5.0	308	2	US-09-595-386-3	Sequence 3, Appl	507	69	5.0	2873	5	PCT-US95-06266-15	Sequence 15, Appl
435	69.5	5.0	308	2	US-09-993-525-3	Sequence 3, Appl	508	68.5	4.9	180	2	US-09-270-767-32589	Sequence 32589, A
436	69.5	5.0	345	2	US-09-543-681A-7546	Sequence 7546, Ap	509	68.5	4.9	241	1	US-08-825-781-3	Sequence 3, Appl
437	69.5	5.0	350	2	US-09-540-236-2338	Sequence 2336, Ap	510	68.5	4.9	264	2	US-09-724-864-64	Sequence 64, Appl
438	69.5	5.0	406	2	US-09-328-352-7149	Sequence 7149, Ap	511	68.5	4.9	300	2	US-09-489-039A-10701	Sequence 10701, A
439	69.5	5.0	417	2	US-09-405-558-44	Sequence 44, Appl	512	68.5	4.9	346	2	US-10-152-886-91	Sequence 91, Appl
440	69.5	5.0	417	2	US-09-538-036-44	Sequence 44, Appl	513	68.5	4.9	346	2	US-09-902-540-14946	Sequence 14946, A
441	69.5	5.0	424	3	US-09-802-208B-5	Sequence 5, Appl	514	68.5	4.9	396	2	US-09-107-532A-4277	Sequence 4277, Ap
442	69.5	5.0	456	2	US-09-489-039A-8332	Sequence 8332, Ap	515	68.5	4.9	396	2	US-09-134-001C-2912	Sequence 2912, Ap
443	69.5	5.0	462	2	US-09-489-039A-13505	Sequence 13505, A	516	68.5	4.9	400	2	US-09-543-681A-6109	Sequence 6109, Ap
444	69.5	5.0	472	2	US-10-154-419-79	Sequence 79, Appl	517	68.5	4.9	402	2	US-09-134-001C-4885	Sequence 4885, Ap
445	69.5	5.0	493	1	US-08-362-512A-4	Sequence 4, Appl	518	68.5	4.9	412	2	US-09-328-352-5543	Sequence 5543, Ap
446	69.5	5.0	493	2	US-08-964-939-4	Sequence 4, Appl	519	68.5	4.9	427	2	US-09-252-991A-29948	Sequence 29948, A
447	69.5	5.0	493	2	US-09-854-774-4	Sequence 4, Appl	520	68.5	4.9	428	2	US-09-328-352-5543	Sequence 5543, Ap
448	69.5	5.0	501	2	US-09-352-991A-28456	Sequence 28456, A	521	68.5	4.9	459	2	US-09-583-110-5017	Sequence 5017, Ap
449	69.5	5.0	513	1	US-09-122-230-7	Sequence 7, Appl	522	68.5	4.9	459	2	US-09-769-787-85	Sequence 85, Appl
450	69.5	5.0	530	2	US-09-540-236-2483	Sequence 2483, Ap	523	68.5	4.9	465	2	US-09-489-039A-7435	Sequence 7435, Ap
451	69.5	5.0	591	2	US-09-643-657-15	Sequence 15, Appl	524	68.5	4.9	470	2	US-09-107-433-4341	Sequence 4341, Ap
452	69.5	5.0	627	2	US-09-538-092-760	Sequence 760, App	525	68.5	4.9	480	2	US-09-305-681-2	Sequence 2, Appl
453	69.5	5.0	653	1	US-07-782-298-2	Sequence 2, Appl	526	68.5	4.9	487	2	US-09-911-132A-4	Sequence 4, Appl
454	69.5	5.0	688	2	US-09-543-681A-4896	Sequence 4896, Ap	527	68.5	4.9	511	2	US-09-305-681-6	Sequence 6, Appl
455	69.5	5.0	1277	2	US-09-397-885-3	Sequence 3, Appl	528	68.5	4.9	538	2	US-09-252-991A-23060	Sequence 23060, A
456	69.5	5.0	1277	2	US-09-969-362-3	Sequence 3, Appl	529	68.5	4.9	541	2	US-09-976-594-931	Sequence 931, App
457	69	5.0	114	2	US-09-134-001C-3376	Sequence 3376, Ap	530	68.5	4.9	549	2	US-09-248-796A-20436	Sequence 20436, A
458	69	5.0	201	2	US-09-605-703B-1952	Sequence 1952, Ap	531	68.5	4.9	661	3	US-10-114-270-142	Sequence 142, App
459	69	5.0	241	2	US-09-328-352-7032	Sequence 7032, Ap	532	68.5	4.9	716	2	US-09-303-518D-108	Sequence 108, App
460	69	5.0	292	2	US-09-370-767-41753	Sequence 41753, A	533	68.5	4.9	1091	2	US-09-306-595C-7	Sequence 7, Appl
461	69	5.0	293	2	US-09-438-185A-313	Sequence 313, App	534	68.5	4.9	1091	2	US-09-925-388-7	Sequence 7, Appl
462	69	5.0	294	2	US-09-902-540-11124	Sequence 11124, A	535	68.5	4.9	1091	2	US-10-431-846-7	Sequence 7, Appl
463	69	5.0	307	2	US-09-605-703B-2582	Sequence 2582, Ap	536	68.5	4.9	2104	1	US-08-808-793-4	Sequence 4, Appl
464	69	5.0	308	2	US-09-198-452A-606	Sequence 606, App	537	68.5	4.9	2104	2	US-08-772-512A-4	Sequence 4, Appl

538	68.5	4.9	2104	2	US-09-428-371-4	Sequence 4, Appli	611	67.5	4.8	940	2	US-09-328-352-8165	Sequence 8165, Ap
539	68.5	4.9	3559	2	US-09-693-205A-10	Sequence 10, Appl	612	67.5	4.8	1084	2	US-09-221-013A-8	Sequence 8, Appli
540	68	4.9	253	2	US-08-858-207A-29	Sequence 299, App	613	67.5	4.8	1326	2	US-09-328-352-4886	Sequence 4886, Ap
541	68	4.9	279	2	US-09-602-787A-558	Sequence 658, App	614	67	4.8	148	2	US-09-270-767-39883	Sequence 39883, A
542	68	4.9	309	2	US-09-710-273-42	Sequence 42, Appl	615	67	4.8	148	2	US-09-270-767-55100	Sequence 55100, A
543	68	4.9	313	2	US-09-583-110-4236	Sequence 4236, Ap	616	67	4.8	162	2	US-09-270-767-45268	Sequence 45268, A
544	68	4.9	315	2	US-09-107-433-3706	Sequence 3706, Ap	617	67	4.8	184	2	US-09-795-926-46	Sequence 46, Appl
545	68	4.9	355	2	US-09-826-509-475	Sequence 475, App	618	67	4.8	184	2	US-10-364-774-46	Sequence 46, Appl
546	68	4.9	379	2	US-09-252-991A-27854	Sequence 27854, A	619	67	4.8	205	2	US-09-252-991A-28363	Sequence 28363, A
547	68	4.9	404	2	US-09-328-352-8182	Sequence 8182, App	620	67	4.8	217	2	US-09-134-000C-6287	Sequence 6287, Ap
548	68	4.9	466	2	US-09-603-208A-236	Sequence 236, App	621	67	4.8	217	4	US-10-038-895A-7	Sequence 7, Appli
549	68	4.9	470	2	US-09-328-352-6673	Sequence 6673, Ap	622	67	4.8	225	2	US-09-543-681A-7698	Sequence 7698, Ap
550	68	4.9	476	2	US-09-328-352-6735	Sequence 6735, Ap	623	67	4.8	277	2	US-09-489-039A-10481	Sequence 10481, A
551	68	4.9	484	2	US-09-134-001C-5063	Sequence 5063, Ap	624	67	4.8	290	2	US-09-248-796A-20347	Sequence 20347, A
552	68	4.9	486	2	US-09-134-001C-3593	Sequence 3593, Ap	625	67	4.8	306	2	US-09-489-039A-10023	Sequence 10023, A
553	68	4.9	503	2	US-09-248-796A-16650	Sequence 16650, A	626	67	4.8	326	2	US-09-543-681A-6673	Sequence 6673, Ap
554	68	4.9	548	2	US-09-328-352-6605	Sequence 6605, Ap	627	67	4.8	345	2	US-09-248-796A-20118	Sequence 20118, A
555	68	4.9	605	2	US-09-583-110-4773	Sequence 4773, Ap	628	67	4.8	359	2	US-09-425-488-2	Sequence 2, Appli
556	68	4.9	619	2	US-09-540-236-2377	Sequence 2377, Ap	629	67	4.8	360	2	US-09-489-039A-8125	Sequence 8125, Ap
557	68	4.9	633	2	US-09-328-352-5439	Sequence 5439, Ap	630	67	4.8	375	2	US-09-543-681A-4465	Sequence 4465, Ap
558	68	4.9	638	1	US-08-295-814B-13	Sequence 13, Appl	631	67	4.8	382	2	US-09-489-039A-10783	Sequence 10783, A
559	68	4.9	638	1	US-08-240-783B-2	Sequence 2, Appli	632	67	4.8	414	2	US-09-334-601-4	Sequence 4, Appli
560	68	4.9	638	2	US-09-084-813-2	Sequence 2, Appli	633	67	4.8	453	1	US-08-439-131A-5	Sequence 5, Appli
561	68	4.9	638	2	US-09-343-361-13	Sequence 13, Appl	634	67	4.8	453	1	US-08-440-674-4	Sequence 4, Appli
562	68	4.9	638	5	FCI-US92-09662-2	Sequence 2, Appli	635	67	4.8	453	2	US-08-879-337-6	Sequence 22, Appl
563	68	4.9	640	2	US-09-627-376-16	Sequence 16, Appl	636	67	4.8	459	2	US-09-097-889-22	Sequence 22, Appl
564	68	4.9	640	2	US-10-047-676B-16	Sequence 16, Appl	637	67	4.8	459	2	US-09-098-079-22	Sequence 22, Appl
565	68	4.9	672	2	US-09-543-681A-5976	Sequence 5976, Ap	638	67	4.8	465	2	US-09-252-991A-19135	Sequence 19135, A
566	68	4.9	694	2	US-09-248-796A-20210	Sequence 20210, A	639	67	4.8	482	2	US-09-489-039A-9369	Sequence 9369, Ap
567	68	4.9	727	2	US-09-543-681A-6690	Sequence 6690, Ap	640	67	4.8	490	2	US-09-328-352-5310	Sequence 5310, Ap
568	68	4.9	783	2	US-09-165-396-2	Sequence 2, Appli	641	67	4.8	494	2	US-09-489-039A-8154	Sequence 8154, Ap
569	68	4.9	905	2	US-09-538-092-1079	Sequence 1079, Ap	642	67	4.8	505	2	US-09-328-352-7155	Sequence 7155, Ap
570	68	4.9	1024	2	US-09-562-737-87	Sequence 87, Appl	643	67	4.8	506	2	US-09-134-000C-6170	Sequence 6170, Ap
571	68	4.9	2864	2	US-08-469-260A-394	Sequence 394, App	644	67	4.8	519	2	US-09-719-919A-17	Sequence 17, Appl
572	68	4.9	2864	2	US-08-488-446-394	Sequence 394, App	645	67	4.8	541	2	US-09-716-129-54	Sequence 54, Appl
573	68	4.9	2864	2	US-08-467-344A-394	Sequence 394, App	646	67	4.8	545	2	US-09-902-540-10576	Sequence 10576, A
574	68	4.9	2864	2	US-08-424-550B-394	Sequence 394, App	647	67	4.8	548	2	US-09-543-681A-4994	Sequence 4994, Ap
575	67.5	4.8	181	2	US-09-270-767-33574	Sequence 33574, A	648	67	4.8	576	2	US-09-540-236-2286	Sequence 2286, Ap
576	67.5	4.8	196	2	US-09-383-586-11	Sequence 11, Appl	649	67	4.8	590	2	US-09-902-540-14944	Sequence 14944, A
577	67.5	4.8	196	2	US-09-823-038A-11	Sequence 11, Appl	650	67	4.8	601	2	US-09-134-000C-5783	Sequence 5783, Ap
578	67.5	4.8	240	2	US-09-540-236-2487	Sequence 2487, Ap	651	67	4.8	608	2	US-09-489-039A-12897	Sequence 12897, A
579	67.5	4.8	249	2	US-09-949-016-7192	Sequence 7192, Ap	652	67	4.8	774	2	US-09-328-352-5361	Sequence 5361, Ap
580	67.5	4.8	264	2	US-09-270-767-41787	Sequence 41787, A	653	67	4.8	878	2	US-10-169-048-42	Sequence 42, Appl
581	67.5	4.8	265	2	US-09-248-796A-17984	Sequence 17984, A	654	67	4.8	1439	1	US-08-449-644-2	Sequence 2, Appli
582	67.5	4.8	299	3	US-10-770-127-139	Sequence 139, App	655	67	4.8	1439	1	US-08-087-244A-2	Sequence 2, Appli
583	67.5	4.8	304	2	US-09-328-352-6103	Sequence 6103, Ap	656	67	4.8	1457	1	US-08-652-971-3	Sequence 3, Appli
584	67.5	4.8	317	2	US-09-489-039A-9602	Sequence 9602, Ap	657	67	4.8	1457	1	US-08-449-644-1	Sequence 1, Appli
585	67.5	4.8	323	2	US-09-107-532A-5460	Sequence 5460, Ap	658	67	4.8	1457	1	US-08-087-244A-1	Sequence 1, Appli
586	67.5	4.8	327	2	US-09-543-681A-6219	Sequence 6219, Ap	659	67	4.8	1457	1	US-08-991-258A-3	Sequence 3, Appli
587	67.5	4.8	336	1	US-08-332-312-4	Sequence 4, Appli	660	67	4.8	1457	1	US-08-769-399-3	Sequence 3, Appli
588	67.5	4.8	360	2	US-09-949-016-10048	Sequence 10048, A	661	67	4.8	1457	2	US-08-991-953A-3	Sequence 3, Appli
589	67.5	4.8	370	2	US-09-303-518D-110	Sequence 110, App	662	66.5	4.8	175	2	US-09-583-110-4664	Sequence 4664, Ap
590	67.5	4.8	411	2	US-09-328-352-5039	Sequence 5039, Ap	663	66.5	4.8	175	2	US-09-769-787-97	Sequence 97, Appl
591	67.5	4.8	421	2	US-09-198-452A-932	Sequence 932, App	664	66.5	4.8	179	2	US-09-107-433-4882	Sequence 4882, Ap
592	67.5	4.8	421	2	US-09-438-185A-869	Sequence 869, App	665	66.5	4.8	243	2	US-09-134-001C-4114	Sequence 4114, Ap
593	67.5	4.8	425	2	US-09-134-000C-5971	Sequence 5971, Ap	666	66.5	4.8	249	2	US-08-858-207A-309	Sequence 309, App
594	67.5	4.8	484	2	US-09-252-991A-32299	Sequence 32299, A	667	66.5	4.8	249	2	US-09-270-767-38186	Sequence 38186, A
595	67.5	4.8	536	2	US-09-107-532A-5507	Sequence 5507, Ap	668	66.5	4.8	249	2	US-09-270-767-53403	Sequence 53403, A
596	67.5	4.8	586	2	US-09-252-991A-24994	Sequence 24994, A	669	66.5	4.8	256	2	US-09-489-039A-9057	Sequence 9057, Ap
597	67.5	4.8	612	2	US-09-248-796A-18040	Sequence 18040, A	670	66.5	4.8	274	2	US-09-830-230A-190	Sequence 190, App
598	67.5	4.8	625	2	US-09-902-540-15330	Sequence 15330, A	671	66.5	4.8	300	2	US-09-393-634-19	Sequence 19, Appl
599	67.5	4.8	632	2	US-09-949-016-10386	Sequence 10386, A	672	66.5	4.8	300	3	US-10-770-127-113	Sequence 113, App
600	67.5	4.8	662	2	US-09-583-110-5119	Sequence 5119, Ap	673	66.5	4.8	306	2	US-09-830-230A-189	Sequence 189, App
601	67.5	4.8	664	2	US-09-107-433-2775	Sequence 2775, Ap	674	66.5	4.8	324	2	US-09-170-496D-196	Sequence 196, App
602	67.5	4.8	667	1	US-07-879-617A-8	Sequence 8, Appli	675	66.5	4.8	329	2	US-09-543-681A-6241	Sequence 6241, Ap
603	67.5	4.8	667	1	US-08-753-985-8	Sequence 8, Appli	676	66.5	4.8	343	2	US-09-543-681A-6853	Sequence 6853, Ap
604	67.5	4.8	680	2	US-09-720-317A-18	Sequence 18, Appl	677	66.5	4.8	349	2	US-09-491-577-96	Sequence 96, Appl
605	67.5	4.8	693	2	US-09-949-016-9666	Sequence 9666, Ap	678	66.5	4.8	380	2	US-09-949-016-10856	Sequence 10856, A
606	67.5	4.8	716	2	US-09-303-518D-112	Sequence 112, App	679	66.5	4.8	392	2	US-09-603-208A-134	Sequence 134, App
607	67.5	4.8	767	2	US-09-328-352-4613	Sequence 4613, Ap	680	66.5	4.8	412	2	US-09-710-279-368	Sequence 368, App
608	67.5	4.8	912	2	US-08-617-785-2	Sequence 2, Appli	681	66.5	4.8	414	2	US-09-605-703B-2352	Sequence 2352, Ap
609	67.5	4.8	912	2	US-09-641-318-2	Sequence 2, Appli	682	66.5	4.8	415	2	US-09-489-039A-10457	Sequence 10457, A
610	67.5	4.8	912	2	US-09-817-464-2	Sequence 2, Appli	683	66.5	4.8	425	2	US-09-543-681A-7042	Sequence 7042, Ap

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685	66.5	4.8	444	2	US-09-694-519-6	Sequence 6, Appli	758	66	4.7	511	2	US-09-345-109C-8	Sequence 8, Appli
686	66.5	4.8	456	2	US-09-328-352-5446	Sequence 5446, Ap	759	66	4.7	536	2	US-09-270-767-44004	Sequence 44004, A
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688	66.5	4.8	488	2	US-09-801-052-5	Sequence 5, Appli	761	66	4.7	620	2	US-09-578-441-4	Sequence 4, Appli
689	66.5	4.8	488	2	US-10-020-121-5	Sequence 5, Appli	762	66	4.7	639	2	US-09-134-001C-5661	Sequence 2, Appli
690	66.5	4.8	488	2	US-10-636-579-5	Sequence 9, Appli	763	66	4.7	687	2	US-08-834-467-2	Sequence 2, Appli
691	66.5	4.8	503	2	US-09-920-262A-9	Sequence 9, Appli	764	66	4.7	687	2	US-09-396-177-2	Sequence 2, Appli
692	66.5	4.8	511	2	US-09-328-352-6365	Sequence 6365, Ap	765	66	4.7	687	2	US-09-248-796A-14715	Sequence 14715, A
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694	66.5	4.8	525	2	US-09-252-991A-23870	Sequence 23870, A	767	66	4.7	856	2	US-10-094-749-2929	Sequence 2929, Ap
695	66.5	4.8	534	2	US-09-107-532A-6592	Sequence 6592, Ap	768	66	4.7	856	2	US-09-248-796A-19088	Sequence 19088, A
696	66.5	4.8	535	2	US-09-107-532A-6593	Sequence 6593, Ap	769	66	4.7	1078	2	US-10-125-772-28	Sequence 28, Appl
697	66.5	4.8	536	2	US-09-809-665A-71	Sequence 71, Appl	770	66	4.7	1078	2	US-10-125-778-28	Sequence 28, Appl
698	66.5	4.8	595	2	US-10-104-047-2714	Sequence 7714, Ap	771	66	4.7	1078	2	US-10-125-792-28	Sequence 28, Appl
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700	66.5	4.8	648	2	US-09-583-110-2729	Sequence 2729, Ap	773	66	4.7	1724	2	US-09-964-899-43	Sequence 43, Appl
701	66.5	4.8	670	2	US-09-107-433-4919	Sequence 4919, Ap	774	66	4.7	4377	2	US-09-949-016-6978	Sequence 6978, Ap
702	66.5	4.8	676	2	US-09-198-452A-836	Sequence 836, Ap	775	65.5	4.7	157	2	US-09-461-325-155	Sequence 155, App
703	66.5	4.8	688	2	US-09-720-317A-2	Sequence 2, Appli	776	65.5	4.7	157	2	US-10-012-542-155	Sequence 155, App
704	66.5	4.8	719	2	US-09-438-185A-788	Sequence 788, App	777	65.5	4.7	157	2	US-10-115-123-155	Sequence 155, App
705	66.5	4.8	736	2	US-09-107-532A-6007	Sequence 6007, Ap	778	65.5	4.7	160	2	US-09-270-757-46920	Sequence 46920, A
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707	66.5	4.8	738	2	US-09-328-352-4315	Sequence 4315, Ap	780	65.5	4.7	239	2	US-09-830-230A-242	Sequence 242, App
708	66.5	4.8	742	2	US-09-107-433-3626	Sequence 3626, Ap	781	65.5	4.7	267	2	US-09-198-452A-231	Sequence 231, App
709	66.5	4.8	755	2	US-09-489-039A-9089	Sequence 9089, Ap	782	65.5	4.7	270	2	US-09-270-767-44001	Sequence 44001, A
710	66.5	4.8	865	2	US-09-252-991A-19339	Sequence 19339, A	783	65.5	4.7	273	2	US-09-830-230A-241	Sequence 241, App
711	66.5	4.8	899	2	US-09-437-568A-48	Sequence 48, Appl	784	65.5	4.7	292	2	US-09-372-422A-4	Sequence 4, Appli
712	66.5	4.8	921	1	US-07-718-575-14	Sequence 14, Appl	785	65.5	4.7	300	2	US-09-303-518D-542	Sequence 542, App
713	66.5	4.8	921	1	US-08-481-206-14	Sequence 14, Appl	786	65.5	4.7	305	2	US-09-107-433-3400	Sequence 3400, Ap
714	66.5	4.8	921	1	US-08-486-269A-14	Sequence 14, Appl	787	65.5	4.7	310	2	US-09-328-352-8117	Sequence 8117, Ap
715	66.5	4.8	1059	2	US-10-160-719A-2	Sequence 2, Appli	788	65.5	4.7	323	2	US-09-134-001C-4635	Sequence 4635, Ap
716	66.5	4.8	1059	2	US-10-209-059-42	Sequence 42, Appl	789	65.5	4.7	329	2	US-09-740-035-2	Sequence 2, Appli
717	66.5	4.8	1148	2	US-09-900-237-4	Sequence 4, Appli	790	65.5	4.7	329	2	US-09-710-279-1942	Sequence 1942, Ap
718	66.5	4.8	1167	2	US-09-008-097-6	Sequence 6, Appli	791	65.5	4.7	332	3	US-10-770-127-101	Sequence 101, App
719	66.5	4.8	1167	2	US-09-472-667-6	Sequence 6, Appli	792	65.5	4.7	344	2	US-09-134-001C-5567	Sequence 5567, Ap
720	66.5	4.8	1548	2	US-10-418-036-14	Sequence 14, Appl	793	65.5	4.7	355	1	US-08-153-848-28	Sequence 28, Appl
721	66.5	4.8	1684	2	US-08-665-259-25	Sequence 25, Appl	794	65.5	4.7	355	1	US-08-153-848-32	Sequence 32, Appl
722	66.5	4.8	1684	2	US-08-762-500-25	Sequence 25, Appl	795	65.5	4.7	355	2	US-09-299-843A-28	Sequence 28, Appl
723	66.5	4.8	1704	2	US-08-762-500-75	Sequence 75, Appl	796	65.5	4.7	355	2	US-09-299-843A-32	Sequence 32, Appl
724	66.5	4.8	1704	2	US-09-032-438C-120	Sequence 120, App	797	65.5	4.7	355	2	US-09-088-337B-32	Sequence 32, Appl
725	66.5	4.8	1766	2	US-09-949-016-10796	Sequence 16, Appl	798	65.5	4.7	355	2	US-09-088-337B-32	Sequence 32, App
726	66	4.7	171	2	US-09-107-383-16	Sequence 16, Appl	799	65.5	4.7	355	2	US-09-170-496D-130	Sequence 130, App
727	66	4.7	171	2	US-09-643-914-16	Sequence 16, Appl	800	65.5	4.7	355	2	US-09-917-254-68	Sequence 68, Appl
728	66	4.7	171	2	US-09-742-361A-16	Sequence 16, Appl	801	65.5	4.7	355	5	PCT-US93-11153-28	Sequence 28, Appl
729	66	4.7	191	2	US-09-443-041A-24	Sequence 24, Appl	802	65.5	4.7	355	5	PCT-US93-11153-32	Sequence 32, Appl
730	66	4.7	216	2	US-10-224-880D-24	Sequence 24, Appl	803	65.5	4.7	356	2	US-09-107-532A-4245	Sequence 4245, Ap
731	66	4.7	254	2	US-09-902-540-15766	Sequence 15766, A	804	65.5	4.7	391	2	US-09-107-532A-4209	Sequence 4209, Ap
732	66	4.7	260	2	US-09-443-041A-10	Sequence 10, Appl	805	65.5	4.7	391	2	US-09-543-681A-7029	Sequence 7029, Ap
733	66	4.7	260	2	US-10-224-880D-10	Sequence 10, Appl	806	65.5	4.7	391	2	US-09-248-796A-15698	Sequence 15698, A
734	66	4.7	281	2	US-09-134-001C-4763	Sequence 4763, Ap	807	65.5	4.7	393	2	US-09-351-150A-29	Sequence 29, Appl
735	66	4.7	345	2	US-09-352-991A-28113	Sequence 28113, A	808	65.5	4.7	393	2	US-09-328-352-8043	Sequence 8043, Ap
736	66	4.7	357	1	US-08-846-762-93	Sequence 93, Appl	809	65.5	4.7	399	2	US-09-560-761B-4	Sequence 4, Appli
737	66	4.7	357	2	US-09-303-518D-850	Sequence 850, App	810	65.5	4.7	399	2	US-09-560-761B-4	Sequence 4, Appli
738	66	4.7	367	2	US-09-134-001C-5557	Sequence 5557, Ap	811	65.5	4.7	422	7	5268463-8	Patent No. 5268463
739	66	4.7	393	2	US-09-134-001C-5594	Sequence 5594, Ap	812	65.5	4.7	426	7	5268463-8	Patent No. 5268463
740	66	4.7	400	2	US-09-198-452A-302	Sequence 302, App	813	65.5	4.7	427	1	US-09-438-185A-217	Sequence 217, App
741	66	4.7	400	2	US-09-438-185A-231	Sequence 231, App	814	65.5	4.7	428	1	US-08-570-157-5	Sequence 5, Appli
742	66	4.7	403	2	US-09-489-039A-11910	Sequence 11910, A	815	65.5	4.7	428	2	US-08-029-170-31	Sequence 31, Appl
743	66	4.7	415	2	US-09-080-044-6	Sequence 6, Appli	816	65.5	4.7	428	2	US-09-076-510-5	Sequence 5, Appli
744	66	4.7	415	2	US-09-531-857A-6	Sequence 6, Appli	817	65.5	4.7	428	2	US-09-004-349-5	Sequence 5, Appli
745	66	4.7	431	5	PCT-US91-00909-6	Sequence 6, Appli	818	65.5	4.7	428	2	US-09-443-745-31	Sequence 31, Appl
746	66	4.7	432	2	US-09-489-039A-7223	Sequence 7223, Ap	819	65.5	4.7	437	2	US-09-489-039A-8958	Sequence 8958, Ap
747	66	4.7	439	2	US-09-248-796A-20082	Sequence 20082, A	820	65.5	4.7	444	1	US-07-937-609-14	Sequence 14, Appl
748	66	4.7	464	2	US-09-252-991A-18525	Sequence 18525, A	821	65.5	4.7	444	2	US-08-029-170-14	Sequence 14, Appl
749	66	4.7	469	2	US-10-094-749-2536	Sequence 2536, Ap	822	65.5	4.7	444	2	US-09-443-745-14	Sequence 14, Appl
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751	66	4.7	481	2	US-09-762-278-4	Sequence 4, Appli	824	65.5	4.7	457	2	US-09-151-957-6	Sequence 6, Appli
752	66	4.7	483	2	US-09-107-532A-4123	Sequence 4123, Ap	825	65.5	4.7	457	2	US-10-195-518-6	Sequence 6, Appli
753	66	4.7	486	2	US-09-489-039A-7706	Sequence 7706, Ap	826	65.5	4.7	465	2	US-09-328-352-5222	Sequence 5222, Ap
754	66	4.7	508	2	US-09-328-352-6467	Sequence 6467, Ap	827	65.5	4.7	490	2	US-09-252-991A-27210	Sequence 27210, A
755	66	4.7	511	2	US-08-278-635B-8	Sequence 8, Appli	828	65.5	4.7	511	2	US-09-305-681-4	Sequence 4, Appli
756	66	4.7	511	2	US-08-464-258B-8	Sequence 8, Appli	829	65.5	4.7	530	2	US-09-134-001C-4510	Sequence 4510, Ap

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831	65.5	4.7	600	2	US-09-438-185A-1013	Sequence 1013, Ap	904	65	4.7	518	2	US-09-548-373D-2	Sequence 2, Appli
832	65.5	4.7	601	1	US-07-676-174A-2	Sequence 2, Appli	905	65	4.7	518	2	US-09-795-847B-2	Sequence 2, Appli
833	65.5	4.7	697	2	US-09-603-208A-226	Sequence 226, Ap	906	65	4.7	518	2	US-09-869-414-2	Sequence 2, Appli
834	65.5	4.7	705	2	US-09-547-789-5	Sequence 5, Appli	907	65	4.7	518	2	US-09-548-368F-2	Sequence 2, Appli
835	65.5	4.7	881	2	US-09-949-016-7764	Sequence 7764, Ap	908	65	4.7	518	2	US-09-548-368D-2	Sequence 2, Appli
836	65.5	4.7	908	2	US-08-855-146-2	Sequence 2, Appli	909	65	4.7	518	2	US-09-794-925A-2	Sequence 2, Appli
837	65.5	4.7	1016	2	US-09-180-439-8	Sequence 8, Appli	910	65	4.7	518	2	US-09-806-194A-2	Sequence 2, Appli
838	65.5	4.7	1036	1	US-08-720-884A-5	Sequence 5, Appli	911	65	4.7	518	2	US-09-668-314C-2	Sequence 2, Appli
839	65.5	4.7	1036	2	US-08-953-823A-5	Sequence 5, Appli	912	65	4.7	518	2	US-09-668-314C-66	Sequence 66, Appli
840	65.5	4.7	1036	2	US-09-398-239-5	Sequence 5, Appli	913	65	4.7	518	2	US-09-548-365-2	Sequence 2, Appli
841	65.5	4.7	1036	2	US-09-560-876A-5	Sequence 5, Appli	914	65	4.7	518	2	US-09-794-743-2	Sequence 2, Appli
842	65.5	4.7	1065	2	US-09-560-876A-6	Sequence 6, Appli	915	65	4.7	518	2	US-09-999-833A-196	Sequence 196, Appli
843	65	4.7	139	2	US-09-902-540-14543	Sequence 14543, A	916	65	4.7	518	2	US-10-020-445A-196	Sequence 196, App
844	65	4.7	144	2	US-09-134-001C-3102	Sequence 3102, Ap	917	65	4.7	518	2	US-09-978-189-196	Sequence 196, App
845	65	4.7	154	2	US-09-955-732A-7	Sequence 7, Appli	918	65	4.7	518	3	US-10-017-085A-196	Sequence 196, App
846	65	4.7	168	2	US-09-544-716-15	Sequence 15, Appli	919	65	4.7	518	3	US-10-145-123A-196	Sequence 196, App
847	65	4.7	168	2	US-09-557-921-16	Sequence 16, Appli	920	65	4.7	518	3	US-10-013-929A-196	Sequence 196, App
848	65	4.7	168	2	US-09-564-357-18	Sequence 18, Appli	921	65	4.7	518	3	US-10-013-917A-196	Sequence 196, App
849	65	4.7	168	2	US-09-619-380-17	Sequence 17, Appli	922	65	4.7	518	3	US-09-489-039A-13906	Sequence 13906, A
850	65	4.7	168	2	US-09-544-517-17	Sequence 17, Appli	923	65	4.7	518	1	US-08-967-101-166	Sequence 166, App
851	65	4.7	168	2	US-09-527-376-12	Sequence 12, Appli	924	65	4.7	541	1	US-08-592-541-166	Sequence 166, App
852	65	4.7	168	2	US-09-775-925-27	Sequence 27, Appli	925	65	4.7	541	2	US-08-888-077A-21	Sequence 21, Appli
853	65	4.7	168	3	US-10-655-073-17	Sequence 17, Appli	926	65	4.7	541	2	US-09-124-698-166	Sequence 166, App
854	65	4.7	198	2	US-09-213-293D-9	Sequence 9, Appli	927	65	4.7	541	2	US-09-127-480-166	Sequence 166, App
855	65	4.7	202	2	US-09-107-433-3144	Sequence 3144, Ap	928	65	4.7	541	2	US-09-124-523-166	Sequence 166, App
856	65	4.7	274	2	US-09-489-039A-14140	Sequence 14140, Ap	929	65	4.7	541	2	US-09-636-796A-166	Sequence 166, App
857	65	4.7	306	2	US-09-248-796A-17619	Sequence 17619, A	930	65	4.7	541	2	US-09-949-016-11075	Sequence 11075, A
858	65	4.7	313	1	US-08-990-379-7	Sequence 7, Appli	931	65	4.7	545	2	US-09-198-452A-519	Sequence 519, App
859	65	4.7	314	2	US-09-164-193-22	Sequence 22, Appli	932	65	4.7	545	2	US-09-438-185A-483	Sequence 483, App
860	65	4.7	314	2	US-09-221-448A-22	Sequence 22, Appli	933	65	4.7	562	2	US-09-328-352-4694	Sequence 4694, Ap
861	65	4.7	315	2	US-09-393-634-56	Sequence 56, Appli	934	65	4.7	574	2	US-09-107-433-3877	Sequence 3877, Ap
862	65	4.7	315	2	US-09-370-767-45996	Sequence 45996, A	935	65	4.7	599	1	US-08-223-619-2	Sequence 2, Appli
863	65	4.7	331	2	US-09-252-991A-24546	Sequence 24546, A	936	65	4.7	599	5	US-08-221-767-24	Sequence 24, Appli
864	65	4.7	332	2	US-09-232-338-8	Sequence 8, Appli	937	65	4.7	599	5	PCT-US95-04075-2	Sequence 2, Appli
865	65	4.7	346	2	US-09-710-279-504	Sequence 504, App	938	65	4.7	617	2	US-10-154-419-52	Sequence 52, Appli
866	65	4.7	356	2	US-09-107-532A-6286	Sequence 6286, Ap	939	65	4.7	633	2	US-09-248-796A-20407	Sequence 20407, A
867	65	4.7	358	2	US-10-104-047-3307	Sequence 3307, Ap	940	65	4.7	732	2	US-09-744-926-2	Sequence 2, Appli
868	65	4.7	367	2	US-09-252-991A-31459	Sequence 31459, A	941	65	4.7	738	2	US-09-107-532A-5096	Sequence 5096, Ap
869	65	4.7	371	2	US-09-540-236-3247	Sequence 3247, Ap	942	65	4.7	768	2	US-09-120-653D-5	Sequence 5, Appli
870	65	4.7	380	2	US-09-489-039A-8153	Sequence 8153, Ap	943	65	4.7	856	2	US-10-099-322-116	Sequence 116, App
871	65	4.7	383	2	US-09-710-279-2026	Sequence 2026, Ap	944	65	4.7	856	2	US-10-044-564-116	Sequence 116, App
872	65	4.7	387	2	US-09-710-279-3180	Sequence 3180, Ap	945	65	4.7	1095	2	US-09-636-215-780	Sequence 780, App
873	65	4.7	390	2	US-09-710-279-1422	Sequence 1422, Ap	946	65	4.7	1095	2	US-09-685-166A-780	Sequence 780, App
874	65	4.7	393	2	US-09-134-000C-4238	Sequence 4238, Ap	947	65	4.7	1095	2	US-09-679-426-780	Sequence 780, App
875	65	4.7	404	2	US-09-710-279-1204	Sequence 1204, Ap	948	65	4.7	1095	2	US-09-759-143-780	Sequence 780, App
876	65	4.7	405	2	US-09-543-681A-4311	Sequence 4311, Ap	949	65	4.7	1095	2	US-09-651-236-780	Sequence 780, App
877	65	4.7	416	2	US-09-134-001C-4084	Sequence 4084, Ap	950	65	4.7	1095	2	US-09-657-279-780	Sequence 780, App
878	65	4.7	405	2	US-09-134-001C-5101	Sequence 5101, Ap	951	65	4.7	1095	2	US-10-012-896-780	Sequence 780, App
879	65	4.7	423	2	US-09-824-551-2	Sequence 3025, A	952	65	4.7	1104	3	US-10-144-678A-780	Sequence 780, App
880	65	4.7	426	2	US-09-252-991A-30025	Sequence 30025, A	953	65	4.7	1104	2	US-09-793-998-11	Sequence 11, Appli
881	65	4.7	433	2	US-09-949-016-8065	Sequence 8065, Ap	954	65	4.7	3174	1	US-08-477-451-3	Sequence 3, Appli
882	65	4.7	436	2	US-09-583-110-4729	Sequence 4729, Ap	955	64.5	4.6	157	2	US-09-605-703B-1500	Sequence 1500, Ap
883	65	4.7	440	2	US-09-107-433-5201	Sequence 5201, Ap	956	64.5	4.6	173	2	US-09-270-767-33313	Sequence 33313, A
884	65	4.7	446	2	US-09-134-000C-6454	Sequence 6454, Ap	957	64.5	4.6	173	2	US-09-270-767-48530	Sequence 48530, A
885	65	4.7	447	2	US-10-094-749-2670	Sequence 2670, Ap	958	64.5	4.6	238	2	US-09-134-001C-3136	Sequence 3136, Ap
886	65	4.7	459	2	US-09-489-039A-9027	Sequence 9027, Ap	959	64.5	4.6	240	2	US-09-543-681A-5483	Sequence 5483, Ap
887	65	4.7	472	2	US-09-489-039A-13479	Sequence 13479, A	960	64.5	4.6	256	2	US-10-104-047-2400	Sequence 2400, Ap
888	65	4.7	482	2	US-09-902-540-10594	Sequence 10594, A	961	64.5	4.6	259	2	US-09-489-039A-11949	Sequence 11949, A
889	65	4.7	490	2	US-09-134-001C-5116	Sequence 5116, Ap	962	64.5	4.6	260	2	US-08-983-075D-9	Sequence 9, Appli
890	65	4.7	494	2	US-09-543-681A-7033	Sequence 7033, Ap	963	64.5	4.6	262	2	US-09-949-016-10927	Sequence 10927, A
891	65	4.7	503	2	US-09-134-001C-3096	Sequence 3096, Ap	964	64.5	4.6	276	2	US-09-583-110-5031	Sequence 5031, Ap
892	65	4.7	505	2	US-09-134-000C-5340	Sequence 5340, Ap	965	64.5	4.6	284	2	US-09-107-433-3147	Sequence 3147, Ap
893	65	4.7	515	2	US-09-489-039A-12306	Sequence 12306, A	966	64.5	4.6	323	2	US-09-489-039A-7408	Sequence 7408, Ap
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895	65	4.7	518	2	US-09-434-427-2	Sequence 2, Appli	968	64.5	4.6	338	2	US-09-270-767-50191	Sequence 50191, A
896	65	4.7	518	2	US-09-548-372D-2	Sequence 2, Appli	969	64.5	4.6	344	2	US-08-311-731A-1702	Sequence 172, App
897	65	4.7	518	2	US-09-548-367D-2	Sequence 2, Appli	970	64.5	4.6	381	2	US-09-248-796A-20097	Sequence 20097, A
898	65	4.7	518	2	US-09-551-853D-2	Sequence 2, Appli	971	64.5	4.6	398	2	US-09-348-930A-9	Sequence 9, Appli
899	65	4.7	518	2	US-09-215-450-19	Sequence 19, Appli	972	64.5	4.6	398	2	US-09-578-063-75	Sequence 75, Appli
900	65	4.7	518	2	US-09-416-901B-2	Sequence 2, Appli	973	64.5	4.6	398	3	US-09-333-159-75	Sequence 75, Appli
901	65	4.7	518	2	US-09-548-376D-2	Sequence 2, Appli	974	64.5	4.6	399	2	US-09-328-352-7394	Sequence 7394, Ap
902	65	4.7	518	2	US-09-886-143-2	Sequence 2, Appli	975	64.5	4.6	404	2	US-09-489-039A-8947	Sequence 8947, Ap

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977	64.5	4.6	411	2	US-09-527-431-80	Sequence 80, Appl	1050	64	4.6	389	1	US-08-846-705-2	Sequence 2, Appl
978	64.5	4.6	411	2	US-09-446-861-80	Sequence 80, Appl	1051	64	4.6	389	2	US-08-211-823C-23	Sequence 23, Appl
979	64.5	4.6	412	2	US-09-198-452A-901	Sequence 90, Appl	1052	64	4.6	392	2	US-09-710-279-3292	Sequence 3292, Ap
980	64.5	4.6	413	2	US-09-438-185A-838	Sequence 838, App	1053	64	4.6	398	2	US-09-489-039A-13159	Sequence 13159, A
981	64.5	4.6	416	2	US-09-540-236-2393	Sequence 2393, Ap	1054	64	4.6	402	2	US-08-846-704-4	Sequence 4, Appl
982	64.5	4.6	431	2	US-09-900-237-28	Sequence 28, Appl	1055	64	4.6	402	2	US-08-462-509B-2	Sequence 2, Appl
983	64.5	4.6	436	2	US-09-949-016-11448	Sequence 11448, A	1056	64	4.6	402	5	PCT-US95-05616-2	Sequence 2, Appl
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986	64.5	4.6	462	2	US-09-902-540-10036	Sequence 10036, A	1059	64	4.6	425	2	US-09-479-128-2	Sequence 2, Appl
987	64.5	4.6	470	1	US-08-724-394A-10	Sequence 10, Appl	1060	64	4.6	425	2	US-09-211-823C-22	Sequence 22, Appl
988	64.5	4.6	493	2	US-09-489-039A-13709	Sequence 13709, A	1061	64	4.6	425	2	US-09-836-509-549	Sequence 549, App
989	64.5	4.6	517	2	US-09-815-923-16	Sequence 16, Appl	1062	64	4.6	428	2	US-09-345-236B-62	Sequence 62, Appl
990	64.5	4.6	534	2	US-09-252-991A-31719	Sequence 31719, A	1063	64	4.6	430	1	US-08-601-435-2	Sequence 2, Appl
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992	64.5	4.6	539	2	US-09-115-150-4	Sequence 4, Appl	1065	64	4.6	430	1	US-08-783-202-2	Sequence 2, Appl
993	64.5	4.6	549	2	US-09-489-039A-8237	Sequence 8237, Ap	1066	64	4.6	430	2	US-09-443-041A-31	Sequence 31, Appl
994	64.5	4.6	549	2	US-09-721-870-18	Sequence 18, Appl	1067	64	4.6	430	2	US-10-224-880D-31	Sequence 31, Appl
995	64.5	4.6	550	2	US-09-543-681A-4582	Sequence 4582, Ap	1068	64	4.6	441	2	US-09-583-110-4400	Sequence 4400, Ap
996	64.5	4.6	555	2	US-09-724-394A-10	Sequence 10, Appl	1069	64	4.6	445	2	US-09-107-433-5039	Sequence 5039, Ap
997	64.5	4.6	561	2	US-09-134-000C-4759	Sequence 4759, Ap	1070	64	4.6	450	2	US-09-107-532A-6507	Sequence 6507, Ap
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1002	64.5	4.6	674	2	US-09-540-236-3546	Sequence 3546, Ap	1075	64	4.6	476	2	US-09-134-001C-3778	Sequence 3778, Ap
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1004	64.5	4.6	723	3	US-09-248-796A-15245	Sequence 15245, A	1077	64	4.6	495	2	US-09-915-181A-7	Sequence 7, Appl
1005	64.5	4.6	723	3	US-10-114-270-144	Sequence 144, App	1078	64	4.6	501	2	US-09-328-352-6371	Sequence 6371, Ap
1006	64.5	4.6	741	2	US-09-605-703B-1584	Sequence 1584, Ap	1079	64	4.6	522	2	US-09-902-540-12496	Sequence 12496, A
1007	64.5	4.6	742	2	US-09-902-540-11489	Sequence 11489, A	1080	64	4.6	533	1	US-08-294-872-2	Sequence 2, Appl
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1012	64.5	4.6	908	2	US-08-249-241-2	Sequence 2, Appl	1085	64	4.6	602	2	US-09-605-703B-1200	Sequence 1200, Ap
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1014	64.5	4.6	912	5	PCT-US91-09422-19	Sequence 19, Appl	1087	64	4.6	615	2	US-09-107-532A-6507	Sequence 6507, Ap
1015	64.5	4.6	1071	1	US-08-975-527-1	Sequence 1, Appl	1088	64	4.6	671	2	US-09-328-352-7868	Sequence 7868, Ap
1016	64.5	4.6	1122	2	US-09-489-039A-8554	Sequence 8554, Ap	1089	64	4.6	696	2	US-09-107-532A-4163	Sequence 4163, Ap
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1019	64	4.6	135	2	US-09-270-767-32080	Sequence 32080, A	1092	64	4.6	823	2	US-09-949-016-6852	Sequence 6852, Ap
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1021	64	4.6	179	2	US-09-902-540-11797	Sequence 11797, A	1094	64	4.6	902	2	US-09-949-016-10381	Sequence 4, Appl
1022	64	4.6	205	2	US-09-540-236-2955	Sequence 2955, Ap	1095	64	4.6	1042	2	US-10-043-418-4	Sequence 32, Appl
1023	64	4.6	238	2	US-09-247-155-89	Sequence 89, Appl	1096	64	4.6	1063	2	US-09-512-250C-32	Sequence 32, Appl
1024	64	4.6	238	2	US-09-903-190-89	Sequence 89, Appl	1097	64	4.6	1094	2	US-09-248-796A-14361	Sequence 14361, A
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1026	64	4.6	258	2	US-09-328-352-4425	Sequence 4425, Ap	1099	64	4.6	1318	2	US-09-949-016-10152	Sequence 10152, A
1027	64	4.6	284	2	US-09-107-532A-5290	Sequence 5290, Ap	1100	64	4.6	1551	2	US-09-437-568A-46	Sequence 46, Appl
1028	64	4.6	296	2	US-09-724-623-103	Sequence 103, App	1101	64	4.6	1551	2	US-10-418-036-13	Sequence 12, Appl
1029	64	4.6	296	3	US-10-288-930-103	Sequence 103, App	1102	63.5	4.6	175	2	US-08-858-207A-363	Sequence 363, App
1030	64	4.6	303	3	US-10-770-127-195	Sequence 195, App	1103	63.5	4.6	221	2	US-09-248-796A-16290	Sequence 16290, A
1031	64	4.6	313	3	US-10-770-127-33	Sequence 33, Appl	1104	63.5	4.6	232	2	US-09-902-540-12730	Sequence 12730, A
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1033	64	4.6	332	1	US-08-671-978B-8	Sequence 8, Appl	1106	63.5	4.6	237	2	US-08-767-820A-21	Sequence 21, Appl
1034	64	4.6	344	2	US-09-110-116-4	Sequence 4, Appl	1107	63.5	4.6	237	2	US-08-622-046B-1	Sequence 1, Appl
1035	64	4.6	355	2	US-09-170-496D-164	Sequence 164, App	1108	63.5	4.6	237	2	US-09-100-264-12	Sequence 12, Appl
1036	64	4.6	357	2	US-09-303-518D-848	Sequence 848, App	1109	63.5	4.6	237	2	US-08-843-076D-8	Sequence 8, Appl
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1042	64	4.6	374	2	US-09-534-185-48	Sequence 48, Appl	1115	63.5	4.6	261	2	US-08-767-820A-19	Sequence 19, Appl
1043	64	4.6	374	2	US-09-914-098-58	Sequence 58, Appl	1116	63.5	4.6	261	2	US-08-622-046B-3	Sequence 3, Appl
1044	64	4.6	377	5	PCT-US95-05616-6	Sequence 6, Appl	1117	63.5	4.6	279	2	US-09-252-991A-24283	Sequence 24283, A
1045	64	4.6	380	2	US-09-097-889-25	Sequence 25, Appl	1118	63.5	4.6	284	2	US-09-303-518D-246	Sequence 246, App
1046	64	4.6	380	2	US-09-098-079-25	Sequence 25, Appl	1119	63.5	4.6	288	2	US-09-372-448A-2	Sequence 2, Appl
1047	64	4.6	386	2	US-09-813-133A-2	Sequence 2, Appl	1120	63.5	4.6	289	2	US-09-372-422A-2	Sequence 2, Appl
1048	64	4.6	386	2	US-09-248-796A-16627	Sequence 16627, A	1121	63.5	4.6	309	2	US-09-902-540-11246	Sequence 11246, A

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1123	63.5	4.6	328	2	US-09-489-039A-10986	Sequence 10986, A	1196	63	4.5	253	1	US-08-684-687-4	Sequence 4, Appli
1124	63.5	4.6	332	2	US-09-252-991A-20929	Sequence 20929, A	1197	63	4.5	253	1	US-08-965-688-4	Sequence 4, Appli
1125	63.5	4.6	332	2	US-09-252-991A-31791	Sequence 31791, A	1198	63	4.5	253	1	US-09-260-173-4	Sequence 4, Appli
1126	63.5	4.6	332	2	US-09-980-145-37	Sequence 37, Appl	1199	63	4.5	253	2	US-09-924-703-6	Sequence 6, Appli
1127	63.5	4.6	341	2	US-10-094-749-2185	Sequence 2185, Ap	1200	63	4.5	259	2	US-09-328-352-6237	Sequence 6237, Ap
1128	63.5	4.6	345	2	US-09-248-796A-20780	Sequence 20780, A	1201	63	4.5	259	2	US-09-602-777A-292	Sequence 292, App
1129	63.5	4.6	356	2	US-08-567-882-7	Sequence 7, Appli	1202	63	4.5	273	2	US-09-949-016-8333	Sequence 8333, Ap
1130	63.5	4.6	359	2	US-09-248-796A-17633	Sequence 17633, A	1203	63	4.5	279	2	US-09-489-039A-13210	Sequence 13210, A
1131	63.5	4.6	378	2	US-09-540-236-3528	Sequence 3528, Ap	1204	63	4.5	284	2	US-09-270-767-33635	Sequence 33635, A
1132	63.5	4.6	379	1	US-08-227-108-18	Sequence 18, Appl	1205	63	4.5	284	2	US-09-270-767-48852	Sequence 48852, A
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1134	63.5	4.6	391	2	US-09-489-039A-9791	Sequence 9791, Ap	1207	63	4.5	289	2	US-09-540-236-2019	Sequence 2019, Ap
1135	63.5	4.6	404	1	PCT-US93-10301-7	Sequence 7, Appli	1208	63	4.5	290	2	US-09-910-174B-8	Sequence 8, Appli
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1137	63.5	4.6	405	2	US-09-248-796A-10869	Sequence 10869, A	1210	63	4.5	290	2	US-09-451-291-1	Sequence 1, Appli
1138	63.5	4.6	414	2	US-09-489-039A-10869	Sequence 10869, A	1211	63	4.5	290	2	US-09-645-069-4	Sequence 4, Appli
1139	63.5	4.6	430	2	US-09-583-110-4230	Sequence 4230, Ap	1212	63	4.5	290	2	US-09-915-789A-17	Sequence 17, Appl
1140	63.5	4.6	430	2	US-09-248-796A-14556	Sequence 14556, A	1213	63	4.5	290	2	US-09-644-934-4	Sequence 4, Appli
1141	63.5	4.6	437	2	US-09-107-433-3678	Sequence 3678, Ap	1214	63	4.5	290	2	US-09-875-338-2	Sequence 2, Appli
1142	63.5	4.6	449	2	US-09-949-016-8594	Sequence 8594, Ap	1215	63	4.5	290	3	US-10-115-609-4	Sequence 4, Appli
1143	63.5	4.6	457	2	US-09-721-870-26	Sequence 26, Appl	1216	63	4.5	299	2	US-09-583-110-2991	Sequence 2991, Ap
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1145	63.5	4.6	470	2	US-09-433-681A-4625	Sequence 4625, Ap	1218	63	4.5	345	2	US-09-107-532A-4426	Sequence 4426, Ap
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1147	63.5	4.6	473	1	US-08-440-674-3	Sequence 3, Appli	1220	63	4.5	345	2	US-09-990-444-2	Sequence 2, Appli
1148	63.5	4.6	473	2	US-08-879-337-7	Sequence 7, Appli	1221	63	4.5	345	2	US-09-997-333-2	Sequence 2, Appli
1149	63.5	4.6	473	2	US-09-303-518D-378	Sequence 378, App	1222	63	4.5	345	2	US-09-992-598-2	Sequence 2, Appli
1150	63.5	4.6	476	2	US-09-489-039A-10203	Sequence 10203, A	1223	63	4.5	345	2	US-09-988-735-2	Sequence 2, Appli
1151	63.5	4.6	482	2	US-09-328-352-7784	Sequence 7784, Ap	1224	63	4.5	345	3	US-09-989-726-2	Sequence 2, Appli
1152	63.5	4.6	488	1	US-08-115-365-2	Sequence 2, Appli	1225	63	4.5	345	3	US-09-997-514-2	Sequence 2, Appli
1153	63.5	4.6	488	1	US-08-586-897-2	Sequence 2, Appli	1226	63	4.5	345	3	US-09-989-728-2	Sequence 2, Appli
1154	63.5	4.6	488	2	US-09-826-509-561	Sequence 561, App	1227	63	4.5	345	3	US-09-997-349-2	Sequence 2, Appli
1155	63.5	4.6	521	2	US-08-956-322-4	Sequence 4, Appli	1228	63	4.5	345	3	US-09-997-653-2	Sequence 2, Appli
1156	63.5	4.6	531	2	US-09-489-039A-9781	Sequence 9781, Ap	1229	63	4.5	345	3	US-09-989-232A-2	Sequence 2, Appli
1157	63.5	4.6	534	2	US-09-710-279-920	Sequence 920, App	1230	63	4.5	346	2	US-09-149-476-433	Sequence 433, App
1158	63.5	4.6	542	2	US-09-830-123-2	Sequence 2, Appli	1231	63	4.5	350	2	US-09-902-540-14418	Sequence 14418, A
1159	63.5	4.6	557	2	US-09-902-540-12884	Sequence 12884, A	1232	63	4.5	354	2	US-09-270-767-45287	Sequence 45287, A
1160	63.5	4.6	571	2	US-09-248-796A-20375	Sequence 20375, A	1233	63	4.5	361	2	US-09-543-681A-5180	Sequence 5180, Ap
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1162	63.5	4.6	650	2	US-08-800-291B-4	Sequence 4, Appli	1235	63	4.5	365	2	US-08-834-032A-17	Sequence 17, Appl
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1164	63.5	4.6	652	2	US-08-956-322-2	Sequence 2, Appli	1237	63	4.5	374	2	US-09-721-341-8	Sequence 8, Appli
1165	63.5	4.6	658	2	US-09-492-709A-352	Sequence 352, App	1238	63	4.5	374	2	US-09-721-341-8	Sequence 8, Appli
1166	63.5	4.6	658	2	US-09-538-092-1190	Sequence 1190, Ap	1239	63	4.5	374	2	US-09-549-848B-17	Sequence 17, Appl
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1169	63.5	4.6	716	2	US-09-303-518D-106	Sequence 106, App	1242	63	4.5	391	2	US-09-328-352-6411	Sequence 6411, Ap
1170	63.5	4.6	769	2	US-10-191-436A-8	Sequence 8, Appli	1243	63	4.5	398	2	US-09-489-039A-9416	Sequence 9416, Ap
1171	63.5	4.6	790	2	US-09-543-681A-5459	Sequence 5459, Ap	1244	63	4.5	401	2	US-09-605-703B-2146	Sequence 2146, Ap
1172	63.5	4.6	799	2	US-10-104-047-2335	Sequence 2335, Ap	1245	63	4.5	409	2	US-09-134-001C-4048	Sequence 4048, Ap
1173	63.5	4.6	803	2	US-09-543-681A-6767	Sequence 6767, Ap	1246	63	4.5	422	2	US-09-543-681A-4762	Sequence 4762, Ap
1174	63.5	4.6	850	2	US-09-583-110-4394	Sequence 4394, Ap	1247	63	4.5	424	2	US-09-543-681A-6042	Sequence 6042, Ap
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1176	63.5	4.6	923	2	US-09-397-885-1	Sequence 1, Appli	1249	63	4.5	430	2	US-09-134-000C-4627	Sequence 4627, Ap
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1178	63.5	4.6	1007	2	US-10-104-047-2552	Sequence 2552, Ap	1251	63	4.5	430	1	US-08-677-049-9	Sequence 9, Appli
1179	63.5	4.6	1007	2	US-10-209-059-28	Sequence 28, Appl	1252	63	4.5	438	1	US-08-570-157-6	Sequence 6, Appli
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1181	63.5	4.6	1098	2	US-08-726-214-10	Sequence 4, Appli	1254	63	4.5	443	2	US-09-830-230A-33	Sequence 33, Appl
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1183	63.5	4.6	1895	2	US-09-487-558B-136	Sequence 136, App	1256	63	4.5	454	1	US-08-959-011-3	Sequence 3, Appli
1184	63.5	4.6	2522	2	US-09-251-645-13	Sequence 13, Appl	1257	63	4.5	461	1	US-09-107-532A-6105	Sequence 6105, Ap
1185	63	4.5	118	2	US-09-583-110-4890	Sequence 4890, Ap	1258	63	4.5	468	1	US-09-949-016-6543	Sequence 10465, A
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1189	63	4.5	214	2	US-09-107-532A-5408	Sequence 5408, Ap	1262	63	4.5	506	2	US-09-134-001C-4290	Sequence 2634, Ap
1190	63	4.5	219	1	US-08-186-529-4	Sequence 4, Appli	1263	63	4.5	521	2	US-09-540-236-2634	Sequence 2, Appli
1191	63	4.5	219	1	US-08-640-386A-4	Sequence 4, Appli	1264	63	4.5	554	2	US-09-657-252-2	Sequence 4703, Ap
1192	63	4.5	249	2	US-09-502-540-13089	Sequence 13089, A	1265	63	4.5	580	2		
1193	63	4.5	250	2	US-09-107-532A-6270	Sequence 6270, Ap	1266	63	4.5	597	2		
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1269	63	4.5	629	2	US-09-252-991A-17988	Sequence 17988, A	1342	62.5	4.5	291	2	US-09-949-016-6919	Sequence 6919, Ap
1270	63	4.5	659	2	US-09-252-991A-30353	Sequence 3053, A	1343	62.5	4.5	291	2	US-09-949-016-6213	Sequence 8213, Ap
1271	63	4.5	683	2	US-08-979-847B-208	Sequence 208, App	1344	62.5	4.5	291	3	US-10-770-127-30	Sequence 30, Appl
1272	63	4.5	683	2	US-08-979-847B-210	Sequence 210, App	1345	62.5	4.5	292	2	US-09-543-681A-7918	Sequence 7918, Ap
1273	63	4.5	831	2	US-10-055-364-39	Sequence 39, Appl	1346	62.5	4.5	299	2	US-09-769-787-82	Sequence 82, Appl
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1275	63	4.5	849	2	US-08-720-229-17	Sequence 17, Appl	1348	62.5	4.5	323	2	US-09-540-236-2883	Sequence 2883, Ap
1276	63	4.5	852	2	US-09-319-588C-18	Sequence 18, Appl	1349	62.5	4.5	324	2	US-09-543-681A-5947	Sequence 5947, Ap
1277	63	4.5	852	3	US-10-301-661B-18	Sequence 18, Appl	1350	62.5	4.5	325	2	US-09-107-532A-6542	Sequence 6542, Ap
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1281	63	4.5	1079	2	US-09-489-039A-7502	Sequence 7502, Ap	1354	62.5	4.5	351	2	US-09-949-016-11252	Sequence 11252, A
1282	63	4.5	1168	2	US-09-313-942-24	Sequence 24, Appl	1355	62.5	4.5	351	2	US-09-949-016-11253	Sequence 11253, A
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1285	63	4.5	2227	2	US-08-475-886-4	Sequence 4, Appli	1358	62.5	4.5	361	2	US-09-364-425B-19	Sequence 19, Appl
1286	63	4.5	2227	2	US-08-475-886-6	Sequence 6, Appli	1359	62.5	4.5	361	2	US-09-364-425B-50	Sequence 50, Appl
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1288	63	4.5	2227	2	US-09-653-499-4	Sequence 4, Appli	1361	62.5	4.5	371	2	US-09-685-166A-708	Sequence 708, App
1289	63	4.5	2227	2	US-09-653-499-6	Sequence 6, Appli	1362	62.5	4.5	371	2	US-09-679-426-708	Sequence 708, App
1290	63	4.5	2227	2	US-10-135-988-4	Sequence 4, Appli	1363	62.5	4.5	371	2	US-09-759-143-708	Sequence 708, App
1291	63	4.5	2227	2	US-10-135-988-6	Sequence 6, Appli	1364	62.5	4.5	371	2	US-09-657-279-708	Sequence 708, App
1292	63	4.5	2368	1	US-08-198-446B-15	Sequence 15, Appl	1365	62.5	4.5	371	2	US-09-657-279-708	Sequence 708, App
1293	63	4.5	2368	1	US-08-870-693-15	Sequence 15, Appl	1366	62.5	4.5	371	2	US-10-012-896-708	Sequence 708, App
1294	63	4.5	2910	1	US-08-466-033-183	Sequence 183, App	1367	62.5	4.5	373	2	US-10-144-678A-708	Sequence 708, App
1295	63	4.5	2910	1	US-08-444-733-183	Sequence 183, App	1368	62.5	4.5	373	2	US-09-107-532A-7048	Sequence 7048, Ap
1296	63	4.5	2910	1	US-08-464-134-183	Sequence 183, App	1369	62.5	4.5	376	2	US-09-949-016-7545	Sequence 7545, Ap
1297	63	4.5	2910	1	US-08-461-361-183	Sequence 183, App	1370	62.5	4.5	382	2	US-09-149-045-2	Sequence 2, Appli
1298	63	4.5	2910	1	US-08-485-910-183	Sequence 183, App	1371	62.5	4.5	392	2	US-09-489-039A-12520	Sequence 12520, A
1299	63	4.5	2910	5	PCT-US95-06266-157	Sequence 157, App	1372	62.5	4.5	398	2	US-09-328-352-6136	Sequence 6136, Ap
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1301	62.5	4.5	117	2	US-09-823-153-2	Sequence 2, Appli	1374	62.5	4.5	400	2	US-09-685-166A-852	Sequence 852, App
1302	62.5	4.5	131	2	US-09-302-540-12460	Sequence 12460, A	1375	62.5	4.5	400	2	US-09-679-426-852	Sequence 852, App
1303	62.5	4.5	164	2	US-09-302-540-10754	Sequence 10754, A	1376	62.5	4.5	400	2	US-09-759-143-852	Sequence 852, App
1304	62.5	4.5	176	2	US-09-248-796A-15652	Sequence 15652, A	1377	62.5	4.5	400	2	US-09-651-236-852	Sequence 852, App
1305	62.5	4.5	202	2	US-09-134-001C-5617	Sequence 5617, Ap	1378	62.5	4.5	400	2	US-09-651-236-852	Sequence 852, App
1306	62.5	4.5	202	2	US-09-543-681A-7271	Sequence 7271, Ap	1379	62.5	4.5	400	2	US-09-657-279-852	Sequence 852, App
1307	62.5	4.5	232	2	US-09-710-279-2580	Sequence 2580, Ap	1380	62.5	4.5	400	3	US-10-012-896-852	Sequence 852, App
1308	62.5	4.5	237	1	US-08-096-946-10	Sequence 10, Appl	1381	62.5	4.5	405	2	US-09-489-039A-9411	Sequence 9411, Ap
1309	62.5	4.5	237	2	US-08-768-859A-16	Sequence 16, Appl	1382	62.5	4.5	405	2	US-09-328-352-5147	Sequence 5147, Ap
1310	62.5	4.5	237	2	US-08-767-820A-16	Sequence 16, Appl	1383	62.5	4.5	415	2	US-09-603-208A-286	Sequence 286, App
1311	62.5	4.5	237	2	US-08-622-046B-12	Sequence 12, Appl	1384	62.5	4.5	415	2	US-09-605-703B-2080	Sequence 2080, Ap
1312	62.5	4.5	237	2	US-08-944-483-37	Sequence 37, Appl	1385	62.5	4.5	424	2	US-09-489-039A-9628	Sequence 9628, Ap
1313	62.5	4.5	237	2	US-09-100-264-1	Sequence 1, Appli	1386	62.5	4.5	437	2	US-09-248-796A-16548	Sequence 16548, A
1314	62.5	4.5	237	2	US-08-843-076D-1	Sequence 1, Appli	1387	62.5	4.5	437	2	US-09-830-433A-59	Sequence 59, Appl
1315	62.5	4.5	237	5	PCT-US94-07329-10	Sequence 10, Appl	1388	62.5	4.5	451	2	US-09-446-861-127	Sequence 127, App
1316	62.5	4.5	237	5	PCT-US95-06157-16	Sequence 16, Appl	1389	62.5	4.5	451	2	US-09-925-637-22	Sequence 22, Appl
1317	62.5	4.5	238	2	US-08-768-859A-8	Sequence 8, Appli	1390	62.5	4.5	455	2	US-09-543-681A-5989	Sequence 5989, Ap
1318	62.5	4.5	238	2	US-08-767-820A-8	Sequence 8, Appli	1391	62.5	4.5	458	2	US-09-489-039A-13954	Sequence 13954, A
1319	62.5	4.5	238	2	PCT-US95-06157-8	Sequence 8, Appli	1392	62.5	4.5	461	2	US-09-252-991A-28434	Sequence 28434, A
1320	62.5	4.5	244	2	US-08-768-859A-10	Sequence 10, Appl	1393	62.5	4.5	461	2	US-09-489-039A-9623	Sequence 9623, Ap
1321	62.5	4.5	244	2	US-08-767-820A-10	Sequence 10, Appl	1394	62.5	4.5	465	2	US-09-328-352-4543	Sequence 4543, Ap
1322	62.5	4.5	244	2	US-08-622-046B-16	Sequence 16, Appl	1395	62.5	4.5	467	2	US-08-706-344C-4	Sequence 4, Appli
1323	62.5	4.5	244	2	US-09-100-264-5	Sequence 5, Appli	1396	62.5	4.5	469	2	US-09-328-352-5007	Sequence 5007, Ap
1324	62.5	4.5	244	2	PCT-US95-06157-10	Sequence 10, Appl	1397	62.5	4.5	473	2	US-09-303-518D-380	Sequence 380, App
1325	62.5	4.5	244	5	US-09-936-271C-75	Sequence 75, Appl	1398	62.5	4.5	480	2	US-09-107-532A-6160	Sequence 6160, Ap
1326	62.5	4.5	255	3	US-08-768-859A-6	Sequence 6, Appli	1399	62.5	4.5	484	2	US-09-266-965-17	Sequence 17, Appl
1327	62.5	4.5	261	2	US-08-767-820A-6	Sequence 6, Appli	1400	62.5	4.5	484	2	US-09-489-039A-12980	Sequence 12980, A
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ALIGNMENTS

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; Patent No. 6913919
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deanovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrata, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C53
; CURRENT FILING DATE: 2001-11-15
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; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/062250
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; PRIOR FILING DATE: 1998-04-28
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; PRIOR FILING DATE: 1998-07-09

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; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
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RESULT 3

US-09-997-333-23
; Sequence 23, Application US/09997333
; Patent No. 6953836
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
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; APPLICANT: Grimaldi, J. Christopher
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; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC27
; CURRENT APPLICATION NUMBER: US/09/997,333
; CURRENT FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16

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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 1392; DB 2; Length 266;
Best Local Similarity 100.0%; Pred. No. 1.2e-144;
Matches 266; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 NIAAVLCIATIVYRYKQVHALSPEENVIIKLNKAGLVGLSCLGLSIVANFQKTLFAA 120

QY 121 HVSGAVLTGMSLYNFVQTLISYQMPKHGKQVFWIRLLLVINCGVSALSMLTCSVYL 180
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QY 181 HSGNFGTDLKQKLNWPKDGYVLLHMTTAAEWSMSFSFGFLLTYIRDFOKISLRVEAN 240
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QY 241 LHGLTYDTAPCPINNERTLLSRDI 266
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RESULT 4
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; Sequence 23, Application US/09992598
; Patent No. 6956108
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deonoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
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; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC20
; CURRENT APPLICATION NUMBER: US/09/992,598
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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;; PRIOR APPLICATION NUMBER: 60/091633
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091978
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 1392; DB 2; Length 266;
Best Local Similarity 100.0%; Pred. No. 1.2e-144;
Matches 266; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 NIAAVLCIATYVRYKQVHALSPENVIKLNKAGLVGLSCLGLSIVANFQKTLFAA 120

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Qy 241 LHGLTYDTAPCPINNERTLLSRDI 266
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RESULT 5

US-09-989-735-23
; Sequence 23, Application US/09989735
; Patent No. 6972185
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
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APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
ACIDS Encoding the Same
FILE REFERENCE: P2730PIC61
CURRENT APPLICATION NUMBER: US/09/989,735
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
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PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 1392; DB 2; Length 266;

Best Local Similarity 100.0%; Pred. No. 1.2e-144; Matches 266; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MWVQGLSFLSALVWTSAAFIYSYITAVTLHIDPALPYISDTGTVAPEKCLFGAML 60
DB 1 MWVQGLSFLSALVWTSAAFIYSYITAVTLHIDPALPYISDTGTVAPEKCLFGAML 60
QY 61 NTAAVLCIATIVRYKQVHALSPEENVIIKLNKAGLVGLSCLGLSIVANFQKTLFAA 120
DB 61 NTAAVLCIATIVRYKQVHALSPEENVIIKLNKAGLVGLSCLGLSIVANFQKTLFAA 120
QY 121 HVGAVLTGMSGLYMFVOTILSYOMPKIHGQVFWIRLLLVIMCGVSALSMLTCSVYL 180
DB 121 HVGAVLTGMSGLYMFVOTILSYOMPKIHGQVFWIRLLLVIMCGVSALSMLTCSVYL 180
QY 181 HSGNFGTDLQKLNWPNEDKGYVHLMTTAAEWSMSFSFGFGLTYIRDFQKISLRVEAN 240
DB 181 HSGNFGTDLQKLNWPNEDKGYVHLMTTAAEWSMSFSFGFGLTYIRDFQKISLRVEAN 240
QY 241 LHGLTLYDTAPCPINNRLLSRDI 266
DB 241 LHGLTLYDTAPCPINNRLLSRDI 266

RESULT 6

US-09-989-726-23
Sequence 23, Application US/09989726
Patent No. 7018811
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PLC60
CURRENT APPLICATION NUMBER: US/09/989,726
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
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;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 1392; DB 3; Length 266;
Best Local Similarity 100.0%; Pred. No. 1.2e-144;
Matches 266; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MWFOGGLSFLPSALVINTSAAFISYITAVTLHHIDPALPYISDTGTVAPEKCLFGAML 60
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Db 61 NIAAVLCIATIVRYKQVHALSPENVIKLNKAGVLGILSCGLSIVANFQKTLFAA 120

QY 121 HVSGAVLTFMGSLYMFVQTILSYOMQPKIHQKQVFWIRLLVIVCGVSALMLTCSVL 180
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QY 241 LHGLTLYDTAPCPINNERTRLISRDII 266
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; Patent No. 7019116
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
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; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
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; APPLICANT: Paoni, Nicholas F.
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; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC46
; CURRENT APPLICATION NUMBER: US/09/997,514
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Db	181	HSGNFGTDLEOKLHNWPKDGVVLHMITTAAEWSMSPSFFGFFLTYYIRDFOKISLRVEAN 240
QY	241	LHGLTYDTAPCPINNERTLLSRDI 266
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RESULT 8		
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; Sequence 23, Application US/09989728		
; Patent No. 7029873		
; GENERAL INFORMATION:		
; APPLICANT: Ashkenazi, Avi J.		
; APPLICANT: Baker, Kevin P.		
; APPLICANT: Botstein, David		
; APPLICANT: Desnoyers, Luc		
; APPLICANT: Eaton, Dan L.		
; APPLICANT: Ferrara, Napoleone		
; APPLICANT: Fong, Sherman		
; APPLICANT: Gerber, Hanspeter		
; APPLICANT: Gerritsen, Mary E.		
; APPLICANT: Goddard, Audrey		
; APPLICANT: Godowski, Paul J.		
; APPLICANT: Grimaldi, J. Christopher		
; APPLICANT: Gurney, Austin L.		
; APPLICANT: Kljavin, Ivar J.		
; APPLICANT: Napier, Mary A.		
; APPLICANT: Pan, James		
; APPLICANT: Paoni, Nicholas F.		
; APPLICANT: Roy, Margaret Ann		
; APPLICANT: Stewart, Timothy A.		
; APPLICANT: Tumas, Daniel		
; APPLICANT: Watanabe, Colin K.		
; APPLICANT: Williams, P. Mickey		
; APPLICANT: Wood, William I.		
; APPLICANT: Zhang, Zemin		
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic		
; TITLE OF INVENTION: Acids Encoding the Same		
; FILE REFERENCE: P2730PIC72		
; CURRENT APPLICATION NUMBER: US/09/989,728		
; CURRENT FILING DATE: 2001-11-20		
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Best Local Similarity 100.0%; Pred. No. 1.2e-144;		
Matches 266; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
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69 PRIOR FILING DATE: 1998-07-07
70 PRIOR APPLICATION NUMBER: 60/092182
71 PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 1392; DB 3; Length 266;
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Matches 266; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MWFOGGLSFLPSALVIWTSAAFTSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAML 60

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QY 121 HVSGLVLTFGMSGLYFVOTILSYQMPKIHGKQVFWIRLLLVICWGSALSMLTCSVYL 180
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121 HVSGLVLTFGMSGLYFVOTILSYQMPKIHGKQVFWIRLLLVICWGSALSMLTCSVYL 180
QY 181 HSGNFGTDLQKLNHPDKGVYLVHMITTAASWSMSFSPFGFLYIRDFQKISLRVEAN 240
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181 HSGNFGTDLQKLNHPDKGVYLVHMITTAASWSMSFSPFGFLYIRDFQKISLRVEAN 240
QY 241 LHGLTLYDTAPCPINNERTRLLSRDI 266
Db |||||
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; Sequence 23, Application US/09997349
; Patent No. 7034106
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Faoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C37
; CURRENT APPLICATION NUMBER: US/09/997,349
; CURRENT FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: 60/049787
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;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William I.
;; APPLICANT: Zhang, Zemin
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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Query Match      100.0%; Score 1392; DB 3; Length 266;
Best Local Similarity 100.0%; Pred. No. 1.2e-144;
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; Patent No. 7034136
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
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; APPLICANT: Goddard, Audrey
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; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
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; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C66
; CURRENT APPLICATION NUMBER: US/09/989,293A
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; PRIOR APPLICATION NUMBER: 60/089653
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/089907
; PRIOR FILING DATE: 1998-06-18
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; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: 60/089952
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; PRIOR FILING DATE: 1998-06-22
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; PRIOR FILING DATE: 1998-06-23
; PRIOR APPLICATION NUMBER: 60/090429
; PRIOR FILING DATE: 1998-06-24
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; PRIOR FILING DATE: 1998-06-24
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; PRIOR APPLICATION NUMBER: 60/090695
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; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090862
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/090863

; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/091360
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091478
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091544
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 1392; DB 3; Length 266;
Best Local Similarity 100.0%; Pred. No. 1.2e-144; Mismatches 0; Indels 0; Gaps 0;
Matches 266; Conservative 0;

Qy 1 MMWFOQGLSFLPSALVIWTSAAFIYSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAML 60
Db 1 MMWFOQGLSFLPSALVIWTSAAFIYSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAML 60

Qy 61 NIAAVLCIATYVRYKQVHALSPENVIIKLNKAGLVGLSCLGSLIVANFQKTLFAA 120
Db 61 NIAAVLCIATYVRYKQVHALSPENVIIKLNKAGLVGLSCLGSLIVANFQKTLFAA 120

Qy 121 HVGSAVLTFGMSLYMFVQTILSYQMOPKIHGKQVFWIRLLLVWCGVSALSMLTCSVVL 180
Db 121 HVGSAVLTFGMSLYMFVQTILSYQMOPKIHGKQVFWIRLLLVWCGVSALSMLTCSVVL 180

Qy 181 HSGNFGTDLQKHLHNPEDKGYVHLMTTAAEWSMSFSFFGFFLTYYIRDFQKISURVEAN 240
Db 181 HSGNFGTDLQKHLHNPEDKGYVHLMTTAAEWSMSFSFSFFGFFLTYYIRDFQKISURVEAN 240

Qy 241 LHGLTLYDTAPCPINNERTLLSRDI 266
Db 241 LHGLTLYDTAPCPINNERTLLSRDI 266

RESULT 12
US-09-663-600A-190
; Sequence 190, Application US/09663600A
; Patent No. 6573068
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste
; APPLICANT: Duclert, Aymeric
; APPLICANT: Bouqueloret, Lydie
; TITLE OF INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS
; FILE REFERENCE: 31.US3.CIP
; CURRENT APPLICATION NUMBER: US/09/663,600A
; CURRENT FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: 09/191,997
; PRIOR FILING DATE: 1998-11-13
; PRIOR APPLICATION NUMBER: 60/066,677
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/069,957
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/074,121
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: 60/081,563
; PRIOR FILING DATE: 1998-04-13
; PRIOR APPLICATION NUMBER: 60/096,116
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: 60/099,273
; PRIOR FILING DATE: 1998-09-04
; NUMBER OF SEQ ID NOS: 229
; SOFTWARE: Patent.pm

SEQ ID NO 190
LENGTH: 267
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SIGNAL
LOCATION: -21...-1
US-09-663-600A-190

Query Match 99.7%; Score 1388; DB 2; Length 267;
Best Local Similarity 99.6%; Pred. No. 3.2e-144; Indels 0; Gaps 0;
Matches 265; Conservative 0; Mismatches 1;

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DB 1 MWVFOGSLFSLPSALVIWTSAAFIYSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAML 60

QY 61 NTAAVLCIATIIYRYKQVHALSPENVIKLNKAGLVGLISCLGSLSIIVANFQKTLTFAA 120
DB 61 NTAAVLCIATIIYRYKQVHALSPENVIKLNKAGLVGLISCLGSLSIIVANFQKTLTFAA 120

QY 121 HVSAGVLTGMSGLYMFVOTILSYQMPKHGQVFWIRLLVWCVSALSMLTCSVL 180
DB 121 HVSAGVLTGMSGLYMFVOTILSYQMPKHGQVFWIRLLVWCVSALSMLTCSVL 180

QY 181 HSGNFGTDLQKLNWPNEDKGYVILHMITTAABMSMSFSFFGFLTYIRDFQKISLRVEAN 240
DB 181 HSGNFGTDLQKLNWPNEDKGYVILHMITTAABMSMSFSFFGFLTYIRDFQKISLRVEAN 240

QY 241 LHGLTYDTAPCPINNERTLLSRDI 266
DB 241 LHGLTYDTAPCPINNERTLLSRDI 266

RESULT 13
US-09-663-600A-96
Sequence 96, Application US/09663600A
Patent No. 6573068
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, Jean-Baptiste
APPLICANT: Duclert, Aymeric
TITLE OF INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS
FILE REFERENCE: 31.US3.CIP
CURRENT APPLICATION NUMBER: US/09/663,600A
PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: 09/191,997
PRIOR FILING DATE: 1998-11-13
PRIOR APPLICATION NUMBER: 60/066,677
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/069,957
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/074,121
PRIOR FILING DATE: 1998-02-09
PRIOR APPLICATION NUMBER: 60/081,563
PRIOR FILING DATE: 1998-04-13
PRIOR APPLICATION NUMBER: 60/096,116
PRIOR FILING DATE: 1998-08-10
PRIOR APPLICATION NUMBER: 60/099,273
PRIOR FILING DATE: 1998-09-04
NUMBER OF SEQ ID NOS: 229
SOFTWARE: Patent.pm
SEQ ID NO 96
LENGTH: 172
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SIGNAL
LOCATION: -21...-1
US-09-663-600A-96

Query Match 42.8%; Score 595.5; DB 2; Length 172;
Best Local Similarity 79.4%; Pred. No. 2.4e-57;

Matches 123; Conservative 7; Mismatches 22; Indels 3; Gaps 2;

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DB 1 MWVFOGSLFSLPSALVIWTSAAFIYSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAML 60

QY 61 NTAAVLCIATIIYRYKQVHALSPENVIKLNKAGLVGLISCLGSLSIIVANFQKTLTFAA 120
DB 61 NTAAVLCIATIIYRYKQVHALSPENVIKLNKAGLVGLISCLGSLSIIVANFQKTLTFAA 120

QY 121 HV-SGAVLTGMSGLYMFVOTILSYQMPKHGK 153
DB 121 TCKWSCAYLWYGL-IYYVCSDDHFFLPKCSPKSNGK 154

RESULT 14
US-09-724-864-38
Sequence 38, Application US/09724864
Patent No. 6380362
GENERAL INFORMATION:
APPLICANT: Watson, James D
APPLICANT: Murison, James G
TITLE OF INVENTION: Polynucleotides, polypeptides expressed
FILE REFERENCE: 11000.1050U1
CURRENT APPLICATION NUMBER: US/09/724,864
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: U.S. No. 6380362 60/171,678
PRIOR FILING DATE: 1999-12-23
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 38
LENGTH: 238
TYPE: PRT
ORGANISM: Mouse
US-09-724-864-38

Query Match 34.4%; Score 479.5; DB 2; Length 238;
Best Local Similarity 37.3%; Pred. No. 2.2e-44;
Matches 93; Conservative 56; Mismatches 79; Indels 21; Gaps 3;

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DB 1 MLCFLRGMAFVFLVLTWSSAAFIISYVAVLSGHVNPFLPYISDTGTPPESGIFGMI 60

QY 61 NTAAVLCIATIIYRYKQV-----HALSPENVIKLNKAGLVGLISCLGSLSIIVANFQ 113
DB 61 NFSAFGLAATMYRIKVEKQNETCYFTPTPNLV-----SLALGVCCIGKGIIVANFQ 114

QY 114 KTLTFAAHVSGAVLTGMSGLYMFVOTILSYQMPKHGQVFWIRLLVWCVSALSM 173
DB 115 ELAVPVVHDGGALLAFVCGVVYTLQSIISYKSCQWNSLTTCVHRMAISAVCAAVPM 174

QY 174 LTCSSVLHSGNFGTDLQKLNWPNEDKGYVILHMITTAABMSMSFSFFGFLTYIRDFQK 233
DB 175 IACASLISI-----TKLEWNPKEKDIYHVWSAICEWTVAFGFIFYFLTFIQDFQSV 226

QY 234 SLRVEANLH 242
DB 227 TLURISTEIN 235

RESULT 15
US-09-663-600A-130
Sequence 130, Application US/09663600A
Patent No. 6573068
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, Jean-Baptiste
APPLICANT: Duclert, Aymeric
APPLICANT: Bougueleret, Lydie
TITLE OF INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS
FILE REFERENCE: 31.US3.CIP
CURRENT APPLICATION NUMBER: US/09/663,600A

Search completed: August 28, 2006, 17:43:02
Job time : 69 secs

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OM protein - protein search, using sw model

Run on: August 28, 2006, 17:37:50 ; Search time 34 Seconds
(without alignments)
535.306 Million cell updates/sec

Title: US-10-006-867-2

Perfect score: 1392

Sequence: 1 MWFFQGLSLFSLVWITS.....YDTAPCINNERTLLSRDI 266

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 247503 seqs, 68422524 residues

Total number of hits satisfying chosen parameters: 247503

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

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- 3: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 4: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
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- 8: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1392	100.0	266	US-10-196-749-10	Sequence 10, Appl
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3	1392	100.0	266	US-11-376-673-2	Sequence 2, Appl
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5	151.5	10.9	437	US-11-395-249-66	Sequence 66, Appl
6	99	7.1	187	US-11-293-697-4787	Sequence 4787, Ap
7	93.5	6.7	303	US-11-056-355B-83608	Sequence 83608, A
8	93.5	6.7	379	US-11-056-355B-83607	Sequence 83607, A
9	88	6.3	312	US-11-056-355B-4953	Sequence 4953, Ap
10	88	6.3	313	US-11-056-355B-4952	Sequence 4952, Ap
11	88	6.3	932	US-10-449-902-35289	Sequence 35289, A
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16	85.5	6.1	545	US-11-395-249-26	Sequence 26, Appl
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18	84.5	6.1	271	US-11-056-355B-8562	Sequence 8562, Ap
19	84.5	6.1	288	US-11-056-355B-8561	Sequence 8561, Ap
20	84.5	6.1	278	US-11-056-355B-8560	Sequence 8560, Ap
21	84.5	6.1	370	US-11-174-307B-4896	Sequence 4896, Ap
22	84.5	6.1	453	US-10-196-749-84	Sequence 84, Appl
23	84.5	6.1	479	US-10-449-902-40971	Sequence 40971, A
24	84.5	6.1	515	US-11-330-403-1950	Sequence 1950, Ap
25	83.5	6.0	468	US-11-330-403-18369	Sequence 18369, A

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27	83	6.0	250	7	US-11-056-355B-83609	Sequence 83609, App
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35	81.5	5.9	294	7	US-11-056-355B-62351	Sequence 62351, A
36	81.5	5.9	334	7	US-11-056-355B-62350	Sequence 62350, A
37	81	5.8	342	7	US-11-347-766-34	Sequence 34, Appl
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52	79	5.7	363	7	US-11-056-355B-114162	Sequence 114162, A
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57	79	5.7	468	6	US-10-449-902-47531	Sequence 47531, A
58	78.5	5.6	288	6	US-10-449-902-38626	Sequence 38626, A
59	78.5	5.6	288	6	US-10-449-902-32821	Sequence 32821, A
60	78.5	5.6	288	6	US-10-449-902-42640	Sequence 42640, A
61	78.5	5.6	288	6	US-10-449-902-43060	Sequence 43067, A
62	78.5	5.6	424	7	US-11-056-355B-17925	Sequence 17925, A
63	78.5	5.6	428	7	US-11-056-355B-17924	Sequence 17924, A
64	78.5	5.6	461	7	US-11-056-355B-88784	Sequence 88784, A
65	78.5	5.6	461	7	US-11-056-355B-92540	Sequence 92540, A
66	78.5	5.6	468	7	US-11-056-355B-88783	Sequence 88783, A
67	78.5	5.6	468	7	US-11-056-355B-92539	Sequence 92539, A
68	78.5	5.6	470	7	US-11-330-403-9708	Sequence 9708, Ap
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70	78.5	5.6	498	7	US-11-056-355B-88782	Sequence 88782, A
71	78.5	5.6	498	7	US-11-056-355B-92538	Sequence 92538, A
72	78.5	5.6	624	7	US-11-056-355B-77797	Sequence 77797, A
73	78.5	5.6	630	7	US-11-056-355B-77796	Sequence 77796, A
74	78.5	5.6	793	7	US-11-325-276-18	Sequence 18, Appl
75	78	5.6	233	7	US-11-367-182-15	Sequence 15, Appl
76	78	5.6	309	7	US-11-178-538-55	Sequence 55, Appl
77	78	5.6	309	7	US-11-178-538-62	Sequence 62, Appl
78	78	5.6	349	6	US-10-953-349-14110	Sequence 14110, A
79	78	5.6	349	6	US-11-056-355B-59893	Sequence 59893, A
80	78	5.6	355	6	US-10-953-349-14109	Sequence 14109, A
81	78	5.6	355	6	US-11-056-355B-59892	Sequence 59892, A
82	78	5.6	362	6	US-10-953-349-14108	Sequence 14108, A
83	78	5.6	362	7	US-11-056-355B-59891	Sequence 59891, A
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87	77.5	5.6	392	7	US-11-056-355B-44866	Sequence 44866, A
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91	77.5	5.6	473	7	US-11-056-355B-70692	Sequence 70692, A
92	77.5	5.6	480	7	US-11-056-355B-70691	Sequence 70691, A
93	77.5	5.6	491	7	US-11-056-355B-80245	Sequence 80245, A
94	77.5	5.6	498	7	US-11-056-355B-80244	Sequence 80244, A
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97	77.5	5.6	635	7	US-11-056-355B-44864	Sequence 44864, A
98	77	5.5	313	6	US-10-449-902-49599	Sequence 49599, A

99	77	5.5	354	6	US-10-449-902-43952	Sequence 43952, A	172	72.5	5.2	456	7	US-11-330-403-429	Sequence 429, App
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101	76.5	5.5	211	7	US-11-056-355B-46703	Sequence 46703, A	174	72.5	5.2	461	7	US-11-330-403-12512	Sequence 12512, A
102	76.5	5.5	211	7	US-11-056-355B-47370	Sequence 47370, A	175	72.5	5.2	525	6	US-10-449-902-43268	Sequence 43268, A
103	76.5	5.5	634	6	US-10-449-902-44817	Sequence 44817, A	176	72.5	5.2	525	6	US-10-449-902-50345	Sequence 50345, A
104	76	5.5	236	7	US-11-056-355B-4954	Sequence 4954, Ap	177	72.5	5.2	688	7	US-11-330-403-11383	Sequence 11383, A
105	76	5.5	287	7	US-11-330-403-3241	Sequence 3241, Ap	178	72	5.2	337	7	US-11-347-870-20	Sequence 20, Appl
106	75.5	5.4	228	7	US-11-056-355B-73049	Sequence 73049, A	179	72	5.2	337	7	US-11-296-615-20	Sequence 20, Appl
107	75.5	5.4	282	7	US-11-056-355B-73048	Sequence 73048, A	180	72	5.2	338	7	US-11-204-427-3	Sequence 3, Appl
108	75.5	5.4	439	7	US-11-342-731-4	Sequence 4, Appl	181	72	5.2	344	7	US-11-056-355B-17517	Sequence 17517, A
109	75.5	5.4	476	7	US-11-330-403-5398	Sequence 5398, Ap	182	72	5.2	423	7	US-11-056-355B-17516	Sequence 17516, A
110	75.5	5.4	476	7	US-11-024-544A-172	Sequence 172, App	183	72	5.2	440	7	US-11-056-355B-91630	Sequence 91630, A
111	75.5	5.4	500	7	US-11-190-750-140	Sequence 140, App	184	72	5.2	440	7	US-11-056-355B-95386	Sequence 95386, A
112	75.5	5.4	500	7	US-11-056-355B-113547	Sequence 113547, A	185	72	5.2	442	7	US-11-056-355B-17515	Sequence 17515, A
113	75.5	5.4	530	7	US-11-056-355B-12402	Sequence 12402, A	186	72	5.2	460	6	US-10-449-902-56742	Sequence 56742, A
114	75.5	5.4	545	7	US-11-056-355B-12401	Sequence 12401, A	187	72	5.2	464	7	US-11-330-403-17886	Sequence 17886, A
115	75	5.4	249	7	US-11-056-355B-22220	Sequence 22220, A	188	72	5.2	542	6	US-10-449-902-33358	Sequence 33358, A
116	75	5.4	254	7	US-11-056-355B-22219	Sequence 22219, A	189	72	5.2	542	6	US-10-449-902-42805	Sequence 42805, A
117	75	5.4	258	6	US-10-449-902-43650	Sequence 42650, A	190	72	5.2	542	6	US-10-449-902-43047	Sequence 43047, A
118	74.5	5.4	327	7	US-11-056-355B-102309	Sequence 102309, A	191	72	5.2	542	6	US-10-449-902-51839	Sequence 51839, A
119	74.5	5.4	327	7	US-11-056-355B-113548	Sequence 113548, A	192	72	5.2	582	7	US-11-056-355B-80100	Sequence 80100, A
120	74.5	5.4	339	6	US-10-449-902-56532	Sequence 56532, A	193	71.5	5.1	254	7	US-11-330-403-17896	Sequence 17896, A
121	74.5	5.4	345	7	US-11-056-355B-41823	Sequence 41823, A	194	71.5	5.1	260	6	US-10-471-571A-4750	Sequence 4750, Ap
122	74.5	5.4	347	7	US-11-056-355B-102308	Sequence 102308, A	195	71.5	5.1	363	7	US-11-056-355B-42530	Sequence 42530, A
123	74.5	5.4	347	7	US-11-056-355B-113547	Sequence 113547, A	196	71.5	5.1	382	7	US-11-056-355B-42529	Sequence 42529, A
124	74.5	5.4	411	7	US-11-330-403-7842	Sequence 7842, Ap	197	71.5	5.1	393	6	US-11-056-355B-42528	Sequence 42528, A
125	74.5	5.4	461	7	US-11-056-355B-91798	Sequence 91798, A	198	71.5	5.1	412	6	US-10-471-571A-2744	Sequence 2744, Ap
126	74.5	5.4	461	7	US-11-056-355B-95554	Sequence 95554, A	199	71.5	5.1	460	6	US-10-449-902-48146	Sequence 48146, A
127	74.5	5.4	535	6	US-10-449-902-51331	Sequence 51331, A	200	71.5	5.1	504	6	US-10-449-902-46591	Sequence 46591, A
128	74	5.3	382	6	US-10-449-902-50854	Sequence 50854, A	201	71.5	5.1	504	7	US-11-197-712-379	Sequence 379, App
129	74	5.3	383	6	US-10-953-349-5125	Sequence 5125, Ap	202	71.5	5.1	603	7	US-11-056-355B-50526	Sequence 50526, A
130	74	5.3	385	6	US-10-449-902-49336	Sequence 49336, A	203	71.5	5.1	665	7	US-11-056-355B-50525	Sequence 50525, A
131	74	5.3	404	7	US-11-330-403-4592	Sequence 4592, Ap	204	71.5	5.1	1053	6	US-10-449-902-41514	Sequence 41514, A
132	74	5.3	409	6	US-10-953-349-5124	Sequence 5124, Ap	205	71	5.1	261	6	US-10-196-749-356	Sequence 356, App
133	74	5.3	532	6	US-10-953-349-5123	Sequence 5123, Ap	206	71	5.1	261	7	US-11-101-316-118	Sequence 118, App
134	74	5.3	979	6	US-10-449-902-41275	Sequence 41275, A	207	71	5.1	261	6	US-11-376-673-118	Sequence 118, App
135	73.5	5.3	337	7	US-11-178-538-38	Sequence 38, Appl	208	71	5.1	405	6	US-10-449-902-43622	Sequence 43622, A
136	73.5	5.3	366	7	US-11-056-355B-98357	Sequence 98357, A	209	71	5.1	438	7	US-11-330-403-2109	Sequence 2109, Ap
137	73.5	5.3	366	7	US-11-056-355B-92113	Sequence 92113, A	210	71	5.1	448	7	US-11-330-403-16813	Sequence 16813, A
138	73.5	5.3	370	7	US-11-056-355B-88356	Sequence 88356, A	211	71	5.1	456	7	US-11-056-355B-89701	Sequence 89701, A
139	73.5	5.3	384	7	US-11-056-355B-92112	Sequence 92112, A	212	71	5.1	456	7	US-11-056-355B-93457	Sequence 93457, A
140	73.5	5.3	370	7	US-11-056-355B-88355	Sequence 88355, A	213	71	5.1	457	6	US-10-449-902-51106	Sequence 51106, A
141	73.5	5.3	384	7	US-11-056-355B-92111	Sequence 92111, A	214	71	5.1	457	7	US-11-056-355B-6882	Sequence 6882, Ap
142	73.5	5.3	441	7	US-11-330-403-18115	Sequence 18115, A	215	71	5.1	466	6	US-10-471-571A-5276	Sequence 5276, Ap
143	73.5	5.3	494	7	US-11-056-355B-91629	Sequence 91629, A	216	71	5.1	467	7	US-11-330-403-14572	Sequence 14572, A
144	73.5	5.3	494	7	US-11-056-355B-95385	Sequence 95385, A	217	71	5.1	487	6	US-10-449-902-37219	Sequence 37219, A
145	73.5	5.3	498	6	US-10-471-571A-192	Sequence 192, App	218	71	5.1	488	7	US-11-056-355B-6881	Sequence 6881, Ap
146	73.5	5.3	522	7	US-11-056-355B-91628	Sequence 91628, A	219	71	5.1	502	6	US-10-543-334-2	Sequence 2, Appl
147	73.5	5.3	522	7	US-11-056-355B-95384	Sequence 95384, A	220	71	5.1	506	7	US-11-056-355B-89700	Sequence 89700, A
148	73.5	5.3	811	6	US-10-449-902-44848	Sequence 44848, A	221	71	5.1	506	7	US-11-056-355B-93456	Sequence 93456, A
149	73.5	5.3	1080	7	US-11-056-355B-69790	Sequence 69790, A	222	71	5.1	510	7	US-11-056-355B-6880	Sequence 6880, Ap
150	73.5	5.3	1097	7	US-11-056-355B-69789	Sequence 69789, A	223	71	5.1	531	6	US-10-449-902-31417	Sequence 31417, A
151	73.5	5.3	1128	7	US-11-056-355B-69788	Sequence 69788, A	224	71	5.1	531	6	US-11-056-355B-89699	Sequence 89699, A
152	73	5.2	203	7	US-11-056-355B-72695	Sequence 72695, A	225	71	5.1	569	7	US-11-056-355B-93455	Sequence 93455, A
153	73	5.2	332	6	US-10-953-349-22929	Sequence 22929, A	226	71	5.1	649	7	US-11-056-355B-90301	Sequence 90301, A
154	73	5.2	332	7	US-11-056-355B-54621	Sequence 54621, A	227	71	5.1	649	7	US-11-056-355B-94057	Sequence 94057, A
155	73	5.2	348	6	US-10-953-349-22928	Sequence 22928, A	228	71	5.1	687	7	US-11-218-716-8	Sequence 8, Appl
156	73	5.2	348	7	US-11-056-355B-54620	Sequence 54620, A	229	71	5.1	692	7	US-11-056-355B-90300	Sequence 90300, A
157	73	5.2	353	7	US-11-056-355B-72694	Sequence 72694, A	230	71	5.1	692	7	US-11-056-355B-94056	Sequence 94056, A
158	73	5.2	355	6	US-10-953-349-22927	Sequence 22927, A	231	71	5.1	693	6	US-10-508-928-678	Sequence 678, App
159	73	5.2	355	7	US-11-056-355B-54619	Sequence 54619, A	232	71	5.1	693	7	US-11-218-716-2	Sequence 2, Appl
160	73	5.2	365	6	US-10-449-902-51917	Sequence 51917, A	233	71	5.1	693	7	US-11-218-716-4	Sequence 4, Appl
161	73	5.2	401	7	US-11-056-355B-72693	Sequence 72693, A	234	71	5.1	693	7	US-11-218-716-6	Sequence 6, Appl
162	73	5.2	458	7	US-11-217-529-3	Sequence 3, Appl	235	71	5.1	733	7	US-11-056-355B-90299	Sequence 90299, A
163	73	5.2	458	7	US-11-056-355B-13955	Sequence 13955, A	236	71	5.1	733	7	US-11-056-355B-94055	Sequence 94055, A
164	73	5.2	458	7	US-11-056-355B-18291	Sequence 18291, A	237	71	5.1	819	6	US-10-449-902-46126	Sequence 46126, A
165	72.5	5.2	273	6	US-10-449-902-43863	Sequence 43863, A	238	71	5.1	819	6	US-10-449-902-46126	Sequence 46126, A
166	72.5	5.2	284	7	US-11-056-355B-52749	Sequence 52749, A	239	71	5.1	918	7	US-10-449-902-46754	Sequence 46754, A
167	72.5	5.2	290	7	US-11-056-355B-52748	Sequence 52748, A	240	70.5	5.1	286	7	US-11-056-355B-39702	Sequence 39702, A
168	72.5	5.2	316	7	US-11-056-355B-70765	Sequence 70765, A	241	70.5	5.1	286	7	US-11-056-355B-76085	Sequence 76085, A
169	72.5	5.2	407	7	US-11-330-403-11369	Sequence 11369, A	242	70.5	5.1	287	6	US-11-330-403-7378	Sequence 7378, Ap
170	72.5	5.2	421	6	US-10-953-349-16497	Sequence 16497, A	243	70.5	5.1	287	6	US-10-953-349-9179	Sequence 9179, Ap
171	72.5	5.2	423	6	US-10-953-349-16496	Sequence 16496, A	244	70.5	5.1	287	6	US-10-953-349-9711	Sequence 9711, Ap

245	70.5	5.1	287	7	US-11-056-355B-23005	Sequence 29005, A	318	69.5	5.0	466	6	US-10-449-902-54312	Sequence 54312, A
246	70.5	5.1	287	7	US-11-056-355B-32595	Sequence 32595, A	319	69.5	5.0	472	7	US-11-275-264-2	Sequence 2, Appli
247	70.5	5.1	287	7	US-11-056-355B-41696	Sequence 41696, A	320	69.5	5.0	472	7	US-11-330-403-4886	Sequence 4886, Ap
248	70.5	5.1	287	7	US-11-056-355B-44798	Sequence 44798, A	321	69.5	5.0	472	7	US-11-330-403-15117	Sequence 15117, A
249	70.5	5.1	287	7	US-11-056-355B-84600	Sequence 84600, A	322	69.5	5.0	472	7	US-11-330-403-17706	Sequence 17706, A
250	70.5	5.1	287	7	US-11-056-355B-84604	Sequence 84604, A	323	69.5	5.0	492	7	US-11-330-403-4693	Sequence 4693, Ap
251	70.5	5.1	287	7	US-11-056-355B-98275	Sequence 98275, A	324	69.5	5.0	493	6	US-10-953-349-2205	Sequence 2205, Ap
252	70.5	5.1	287	7	US-11-056-355B-108389	Sequence 108389, A	325	69.5	5.0	493	7	US-11-056-355B-40482	Sequence 40482, A
253	70.5	5.1	287	7	US-11-056-355B-109514	Sequence 109514, A	326	69.5	5.0	493	7	US-11-056-355B-102249	Sequence 102249, A
254	70.5	5.1	287	7	US-11-056-355B-119628	Sequence 119628, A	327	69.5	5.0	493	7	US-11-056-355B-113488	Sequence 113488, A
255	70.5	5.1	319	7	US-11-377-517-6	Sequence 6, Appli	328	69.5	5.0	507	7	US-11-330-403-9565	Sequence 9565, Ap
256	70.5	5.1	319	7	US-11-377-517-7	Sequence 7, Appli	329	69.5	5.0	515	7	US-11-330-403-533	Sequence 533, Ap
257	70.5	5.1	419	6	US-10-471-571A-4350	Sequence 4350, Ap	330	69.5	5.0	525	7	US-11-330-403-15816	Sequence 15816, A
258	70.5	5.1	454	7	US-11-056-355B-91799	Sequence 91799, A	331	69.5	5.0	617	7	US-11-056-355B-42359	Sequence 42359, A
259	70.5	5.1	454	7	US-11-056-355B-95555	Sequence 95555, A	332	69.5	5.0	619	7	US-11-056-355B-42358	Sequence 42358, A
260	70.5	5.1	515	7	US-11-056-355B-81260	Sequence 81260, A	333	69.5	5.0	630	7	US-11-056-355B-42357	Sequence 42357, A
261	70.5	5.1	520	7	US-11-174-307B-5508	Sequence 5508, Ap	334	69.5	5.0	781	7	US-11-330-403-2056	Sequence 2056, Ap
262	70.5	5.1	520	7	US-11-296-657-4	Sequence 4, Appli	335	69.5	5.0	794	7	US-11-330-403-11306	Sequence 11306, A
263	70.5	5.1	525	7	US-11-056-355B-81259	Sequence 81259, A	336	69	5.0	285	7	US-11-330-403-15938	Sequence 15938, A
264	70.5	5.1	533	7	US-11-056-355B-81258	Sequence 81258, A	337	69	5.0	321	7	US-11-332-138-2	Sequence 2, Appli
265	70.5	5.1	546	7	US-11-056-355B-77798	Sequence 77798, A	338	69	5.0	328	7	US-11-056-355B-52854	Sequence 52854, A
266	70.5	5.1	549	7	US-11-056-355B-87887	Sequence 87887, A	339	69	5.0	353	7	US-11-056-355B-77764	Sequence 77764, A
267	70.5	5.1	553	6	US-10-517-552-10	Sequence 10, Appli	340	69	5.0	353	7	US-11-056-355B-85908	Sequence 85908, A
268	70.5	5.1	564	7	US-11-056-355B-87886	Sequence 87886, A	341	69	5.0	366	6	US-10-961-569-2	Sequence 20, Appli
269	70.5	5.1	594	7	US-11-056-355B-87885	Sequence 87885, A	342	69	5.0	366	6	US-10-961-569-20	Sequence 20, Appli
270	70.5	5.1	619	7	US-11-312-958-46	Sequence 46, Appli	343	69	5.0	371	7	US-11-056-355B-77763	Sequence 77763, A
271	70.5	5.1	687	7	US-11-341-947-2	Sequence 2, Appli	344	69	5.0	371	7	US-11-056-355B-85907	Sequence 85907, A
272	70.5	5.1	687	7	US-11-218-716-10	Sequence 10, Appli	345	69	5.0	382	7	US-11-056-355B-90765	Sequence 90765, A
273	70.5	5.1	823	7	US-11-330-403-609	Sequence 609, Appli	346	69	5.0	382	7	US-11-056-355B-94521	Sequence 94521, A
274	70.5	5.1	850	7	US-11-056-355B-75830	Sequence 75830, A	347	69	5.0	389	7	US-11-056-355B-77762	Sequence 77762, A
275	70.5	5.1	861	7	US-11-056-355B-100179	Sequence 100179, A	348	69	5.0	398	6	US-10-449-902-47833	Sequence 47833, A
276	70.5	5.1	861	7	US-11-056-355B-111418	Sequence 111418, A	349	69	5.0	458	7	US-11-056-355B-85906	Sequence 85906, A
277	70.5	5.1	870	7	US-11-056-355B-75829	Sequence 75829, A	350	69	5.0	471	6	US-10-449-902-38797	Sequence 38797, A
278	70.5	5.1	881	7	US-11-056-355B-100178	Sequence 100178, A	351	69	5.0	479	7	US-11-330-403-4766	Sequence 4766, Ap
279	70.5	5.1	881	7	US-11-056-355B-111417	Sequence 111417, A	352	69	5.0	487	6	US-10-471-571A-3798	Sequence 3798, Ap
280	70.5	5.1	886	6	US-10-449-902-43638	Sequence 43638, A	353	69	5.0	492	6	US-10-511-937-2352	Sequence 2952, Ap
281	70.5	5.1	886	6	US-10-449-902-46619	Sequence 46619, A	354	69	5.0	502	6	US-10-545-334-4	Sequence 4, Appli
282	70.5	5.1	1058	7	US-11-056-355B-75828	Sequence 75828, A	355	69	5.0	502	6	US-10-545-334-6	Sequence 6, Appli
283	70.5	5.1	1069	7	US-11-056-355B-100177	Sequence 100177, A	356	69	5.0	527	7	US-11-174-307B-3816	Sequence 3816, Ap
284	70.5	5.1	1069	7	US-11-056-355B-111416	Sequence 111416, A	357	69	5.0	588	7	US-11-233-089-42	Sequence 42, Appli
285	70	5.0	173	6	US-10-953-349-11257	Sequence 11257, A	358	69	5.0	781	7	US-11-330-403-8852	Sequence 8852, Ap
286	70	5.0	173	6	US-11-056-355B-46645	Sequence 46645, A	359	69	5.0	1095	7	US-11-228-554-95	Sequence 95, Appli
287	70	5.0	177	6	US-10-953-349-11256	Sequence 11256, A	360	69	5.0	1095	7	US-11-228-554-96	Sequence 96, Appli
288	70	5.0	177	6	US-11-056-355B-46644	Sequence 46644, A	361	69	5.0	1095	7	US-11-248-718-95	Sequence 95, Appli
289	70	5.0	208	7	US-11-030-653-8	Sequence 8, Appli	362	69	5.0	1295	7	US-11-248-718-96	Sequence 96, Appli
290	70	5.0	218	7	US-11-056-355B-102310	Sequence 102310, A	363	68.5	4.9	226	7	US-11-056-355B-39379	Sequence 39379, A
291	70	5.0	218	7	US-11-056-355B-113549	Sequence 113549, A	364	68.5	4.9	252	7	US-11-056-355B-97611	Sequence 97611, A
292	70	5.0	262	6	US-10-449-902-31380	Sequence 31380, A	365	68.5	4.9	252	7	US-11-056-355B-108850	Sequence 108850, A
293	70	5.0	262	6	US-10-449-902-51444	Sequence 51444, A	366	68.5	4.9	263	7	US-11-056-355B-39378	Sequence 39378, A
294	70	5.0	262	6	US-10-449-902-54914	Sequence 54914, A	367	68.5	4.9	329	7	US-11-056-355B-45626	Sequence 45626, A
295	70	5.0	288	7	US-11-330-403-8004	Sequence 8004, Ap	368	68.5	4.9	329	7	US-11-056-355B-50568	Sequence 50568, A
296	70	5.0	296	6	US-11-330-403-2246	Sequence 2246, Ap	369	68.5	4.9	343	7	US-11-056-355B-45625	Sequence 45625, A
297	70	5.0	364	6	US-10-953-349-16498	Sequence 16498, A	370	68.5	4.9	343	7	US-11-056-355B-50567	Sequence 50567, A
298	70	5.0	364	6	US-10-449-902-49967	Sequence 49967, A	371	68.5	4.9	385	7	US-11-056-355B-24553	Sequence 24553, A
299	70	5.0	512	7	US-11-330-403-12827	Sequence 12827, A	372	68.5	4.9	407	7	US-11-330-403-12810	Sequence 12810, A
300	70	5.0	518	7	US-11-330-403-8770	Sequence 8770, Ap	373	68.5	4.9	415	7	US-11-056-355B-78941	Sequence 78941, A
301	70	5.0	526	6	US-10-953-349-7169	Sequence 7169, Ap	374	68.5	4.9	431	7	US-11-330-403-11168	Sequence 1168, Ap
302	70	5.0	778	6	US-10-449-902-43100	Sequence 43100, A	375	68.5	4.9	435	6	US-10-953-349-7171	Sequence 7171, Ap
303	70	5.0	778	6	US-10-449-902-43438	Sequence 43438, A	376	68.5	4.9	436	6	US-10-953-349-7170	Sequence 7170, Ap
304	70	5.0	905	6	US-10-449-902-31457	Sequence 31457, A	377	68.5	4.9	448	7	US-11-056-355B-78940	Sequence 78940, A
305	69.5	5.0	202	6	US-10-953-349-2415	Sequence 2415, Ap	378	68.5	4.9	454	7	US-11-056-355B-78939	Sequence 78939, A
306	69.5	5.0	202	7	US-11-056-355B-27404	Sequence 27404, A	379	68.5	4.9	483	7	US-11-056-355B-100606	Sequence 100606, A
307	69.5	5.0	202	7	US-11-056-355B-74656	Sequence 74656, A	380	68.5	4.9	483	7	US-11-056-355B-111845	Sequence 111845, A
308	69.5	5.0	226	7	US-11-056-355B-101410	Sequence 101410, A	381	68.5	4.9	502	7	US-11-056-355B-100605	Sequence 100605, A
309	69.5	5.0	226	7	US-11-056-355B-112649	Sequence 112649, A	382	68.5	4.9	502	7	US-11-056-355B-111844	Sequence 111844, A
310	69.5	5.0	247	6	US-10-953-349-2414	Sequence 2414, Ap	383	68.5	4.9	509	7	US-11-056-355B-100604	Sequence 100604, A
311	69.5	5.0	247	7	US-11-056-355B-27403	Sequence 27403, A	384	68.5	4.9	509	7	US-11-056-355B-111843	Sequence 111843, A
312	69.5	5.0	247	7	US-11-056-355B-74655	Sequence 74655, A	385	68.5	4.9	518	6	US-10-449-902-31365	Sequence 31365, A
313	69.5	5.0	261	7	US-11-056-355B-101409	Sequence 101409, A	386	68.5	4.9	592	6	US-10-449-902-38524	Sequence 38524, A
314	69.5	5.0	261	7	US-11-056-355B-112648	Sequence 112648, A	387	68.5	4.9	867	7	US-11-056-355B-75940	Sequence 75940, A
315	69.5	5.0	263	7	US-11-056-355B-101408	Sequence 101408, A	388	68.5	4.9	884	7	US-11-056-355B-91295	Sequence 91295, A
316	69.5	5.0	263	7	US-11-056-355B-112647	Sequence 112647, A	389	68.5	4.9	884	7	US-11-056-355B-95051	Sequence 95051, A
317	69.5	5.0	287	7	US-11-330-403-6433	Sequence 6433, Ap	390	68.5	4.9	907	7	US-11-056-355B-75747	Sequence 75747, A

391	68.5	4.9	925	7	US-11-056-355B-100336	Sequence 100336,	464	67.5	4.8	1054	7	US-11-056-355B-47978	Sequence 47978, A
392	68.5	4.9	925	7	US-11-056-355B-111575	Sequence 111575,	465	67.5	4.8	1054	7	US-11-056-355B-48216	Sequence 48216, A
393	68.5	4.9	939	7	US-11-056-355B-75939	Sequence 75939, A	466	67.5	4.8	1065	7	US-11-056-355B-37324	Sequence 37324, A
394	68.5	4.9	949	7	US-11-056-355B-75746	Sequence 75746, A	467	67.5	4.8	1065	7	US-11-056-355B-47977	Sequence 47977, A
395	68.5	4.9	956	7	US-11-056-355B-91294	Sequence 91294, A	468	67.5	4.8	1065	7	US-11-056-355B-48215	Sequence 48215, A
396	68.5	4.9	956	7	US-11-056-355B-95050	Sequence 95050, A	469	67.5	4.8	1092	6	US-10-449-902-53776	Sequence 53776, A
397	68.5	4.9	967	7	US-11-056-355B-100335	Sequence 100335,	470	67.5	4.8	1201	7	US-11-273-537-31	Sequence 31, Appl
398	68.5	4.9	967	7	US-11-056-355B-111574	Sequence 111574,	471	67.5	4.8	1263	6	US-10-471-571A-5118	Sequence 5118, Appl
399	68.5	4.9	1066	7	US-11-056-355B-75745	Sequence 75745, A	472	67	4.8	250	6	US-10-449-902-40088	Sequence 40088, A
400	68.5	4.9	1067	7	US-11-056-355B-75938	Sequence 75938, A	473	67	4.8	258	7	US-11-056-355B-5154	Sequence 5154, Ap
401	68.5	4.9	1081	7	US-11-325-276-29	Sequence 29, Appl	474	67	4.8	258	7	US-11-056-355B-6210	Sequence 6210, Ap
402	68.5	4.9	1084	7	US-11-056-355B-91293	Sequence 91293, A	475	67	4.8	264	7	US-11-056-355B-5153	Sequence 5153, Ap
403	68.5	4.9	1084	7	US-11-056-355B-95049	Sequence 95049, A	476	67	4.8	264	7	US-11-056-355B-6209	Sequence 6209, Ap
404	68.5	4.9	1084	7	US-11-056-355B-100334	Sequence 100334,	477	67	4.8	265	7	US-11-056-355B-24744	Sequence 24744, A
405	68.5	4.9	1084	7	US-11-056-355B-111573	Sequence 111573,	478	67	4.8	290	6	US-10-471-571A-498	Sequence 498, App
406	68.5	4.9	1084	7	US-11-325-276-24	Sequence 24, Appl	479	67	4.8	292	7	US-11-056-355B-6208	Sequence 6208, Ap
407	68	4.9	217	7	US-11-056-355B-73050	Sequence 73050, A	480	67	4.8	293	7	US-11-330-403-1176	Sequence 1176, Ap
408	68	4.9	265	6	US-10-449-902-54848	Sequence 54848, A	481	67	4.8	293	7	US-11-330-403-1251	Sequence 1251, Ap
409	68	4.9	290	6	US-10-953-349-25004	Sequence 25004, A	482	67	4.8	293	7	US-11-330-403-5047	Sequence 5047, Ap
410	68	4.9	290	6	US-11-056-355B-55296	Sequence 55296, A	483	67	4.8	297	7	US-11-056-355B-5152	Sequence 5152, Ap
411	68	4.9	305	6	US-10-471-571A-2352	Sequence 2352, Ap	484	67	4.8	313	6	US-10-953-349-27376	Sequence 27376, A
412	68	4.9	355	7	US-11-404-939-475	Sequence 475, App	485	67	4.8	313	6	US-11-056-355B-63128	Sequence 63128, A
413	68	4.9	369	7	US-11-056-355B-78288	Sequence 78288, A	486	67	4.8	314	6	US-10-953-349-27375	Sequence 27375, A
414	68	4.9	372	6	US-10-953-349-25003	Sequence 25003, A	487	67	4.8	314	6	US-11-056-355B-63127	Sequence 63127, A
415	68	4.9	372	6	US-11-056-355B-55295	Sequence 55295, A	488	67	4.8	334	7	US-11-056-355B-89673	Sequence 89673, A
416	68	4.9	443	7	US-11-056-355B-100239	Sequence 100239,	489	67	4.8	334	7	US-11-056-355B-93429	Sequence 93429, A
417	68	4.9	443	7	US-11-056-355B-111478	Sequence 111478,	490	67	4.8	334	7	US-11-056-355B-93427	Sequence 93427, A
418	68	4.9	457	7	US-11-330-403-927	Sequence 927, App	491	67	4.8	340	6	US-10-953-349-28000	Sequence 28000, A
419	68	4.9	458	6	US-10-449-902-51682	Sequence 51682, A	492	67	4.8	345	7	US-11-330-403-3922	Sequence 3922, Ap
420	68	4.9	458	6	US-10-449-902-54211	Sequence 54211, A	493	67	4.8	356	7	US-11-056-355B-89672	Sequence 89672, A
421	68	4.9	458	7	US-11-317-789A-438	Sequence 438, App	494	67	4.8	356	7	US-11-056-355B-93428	Sequence 93428, A
422	68	4.9	461	7	US-11-330-403-10235	Sequence 10235, A	495	67	4.8	357	6	US-10-953-349-27374	Sequence 27374, A
423	68	4.9	464	7	US-11-330-403-7208	Sequence 7208, Ap	496	67	4.8	357	6	US-10-953-349-27374	Sequence 27374, A
424	68	4.9	486	6	US-10-449-902-50373	Sequence 50373, A	497	67	4.8	358	7	US-11-056-355B-89671	Sequence 89671, A
425	68	4.9	486	6	US-11-330-403-18338	Sequence 18338, A	498	67	4.8	358	7	US-11-056-355B-93427	Sequence 93427, A
426	68	4.9	493	7	US-11-330-403-7774	Sequence 7774, Ap	499	67	4.8	363	6	US-10-449-902-56364	Sequence 56364, A
427	68	4.9	506	7	US-11-056-355B-100238	Sequence 100238,	500	67	4.8	370	6	US-10-505-928-672	Sequence 672, App
428	68	4.9	506	7	US-11-056-355B-111477	Sequence 111477,	501	67	4.8	370	6	US-10-449-902-55544	Sequence 55544, A
429	68	4.9	510	6	US-10-449-902-46896	Sequence 46896, A	502	67	4.8	397	6	US-10-505-405-22	Sequence 22, Appl
430	68	4.9	532	7	US-11-330-403-1394	Sequence 1394, Ap	503	67	4.8	398	7	US-11-056-355B-2956	Sequence 2956, Ap
431	68	4.9	624	7	US-11-056-355B-100237	Sequence 100237,	504	67	4.8	398	7	US-11-317-789A-439	Sequence 439, App
432	68	4.9	624	7	US-11-056-355B-111476	Sequence 111476,	505	67	4.8	408	6	US-10-953-349-5885	Sequence 5885, Ap
433	68	4.9	722	7	US-11-330-403-8355	Sequence 8355, Ap	506	67	4.8	408	7	US-11-056-355B-34976	Sequence 34976, A
434	68	4.9	905	6	US-10-449-902-42984	Sequence 42984, A	507	67	4.8	408	7	US-11-056-355B-99387	Sequence 99387, A
435	67.5	4.8	171	7	US-11-056-355B-5480	Sequence 5480, Ap	508	67	4.8	408	7	US-11-056-355B-110626	Sequence 110626,
436	67.5	4.8	293	7	US-11-330-403-15524	Sequence 15524, A	509	67	4.8	408	7	US-11-330-403-334	Sequence 334, App
437	67.5	4.8	304	6	US-10-471-571A-4038	Sequence 4038, Ap	510	67	4.8	413	6	US-10-953-349-24222	Sequence 24222, A
438	67.5	4.8	336	6	US-11-178-538-4	Sequence 4, Appl	511	67	4.8	413	6	US-10-953-349-24222	Sequence 24222, A
439	67.5	4.8	365	6	US-10-953-349-28815	Sequence 28815, A	512	67	4.8	413	7	US-11-056-355B-25275	Sequence 25275, A
440	67.5	4.8	365	7	US-11-056-355B-68532	Sequence 68532, A	513	67	4.8	414	7	US-11-056-355B-25274	Sequence 25274, A
441	67.5	4.8	389	6	US-10-953-349-28814	Sequence 28814, A	514	67	4.8	429	6	US-10-953-349-24221	Sequence 24221, A
442	67.5	4.8	389	7	US-11-056-355B-68531	Sequence 68531, A	515	67	4.8	431	6	US-10-953-349-24220	Sequence 24220, A
443	67.5	4.8	443	7	US-11-330-403-16503	Sequence 16503, A	516	67	4.8	459	7	US-11-056-355B-2955	Sequence 2955, Ap
444	67.5	4.8	443	7	US-11-056-355B-41658	Sequence 41658, A	517	67	4.8	459	7	US-11-317-789A-437	Sequence 437, App
445	67.5	4.8	457	7	US-11-056-355B-41659	Sequence 41659, A	518	67	4.8	462	7	US-11-056-355B-25273	Sequence 25273, A
446	67.5	4.8	458	7	US-11-056-355B-41659	Sequence 41659, A	519	67	4.8	473	6	US-10-953-349-11576	Sequence 11576, A
447	67.5	4.8	463	7	US-11-330-403-19149	Sequence 19149, A	520	67	4.8	473	7	US-11-056-355B-48903	Sequence 48903, A
448	67.5	4.8	473	6	US-10-449-902-47556	Sequence 47556, A	521	67	4.8	474	7	US-11-056-355B-85172	Sequence 85172, A
449	67.5	4.8	479	7	US-10-449-902-47556	Sequence 47556, A	522	67	4.8	491	6	US-11-056-355B-85172	Sequence 85172, A
450	67.5	4.8	490	6	US-10-449-902-45547	Sequence 45547, A	523	67	4.8	491	6	US-11-056-355B-84959	Sequence 84959, A
451	67.5	4.8	501	7	US-11-056-355B-41658	Sequence 41658, A	524	67	4.8	507	6	US-10-953-349-25186	Sequence 25186, A
452	67.5	4.8	511	7	US-11-056-355B-83855	Sequence 83855, A	525	67	4.8	508	6	US-10-953-349-25185	Sequence 25185, A
453	67.5	4.8	514	7	US-11-056-355B-37551	Sequence 37551, A	526	67	4.8	520	7	US-11-056-355B-2954	Sequence 2954, Ap
454	67.5	4.8	515	7	US-11-056-355B-83854	Sequence 83854, A	527	67	4.8	521	6	US-11-056-355B-84958	Sequence 84958, A
455	67.5	4.8	532	7	US-11-056-355B-37550	Sequence 37550, A	528	67	4.8	524	6	US-10-953-349-11575	Sequence 11575, A
456	67.5	4.8	578	6	US-10-471-571A-2774	Sequence 2774, Ap	529	67	4.8	524	7	US-11-056-355B-48902	Sequence 48902, A
457	67.5	4.8	717	7	US-11-293-697-3828	Sequence 3828, Ap	530	67	4.8	524	7	US-11-056-355B-78060	Sequence 78060, A
458	67.5	4.8	754	6	US-10-518-941-28	Sequence 28, Appl	531	67	4.8	527	7	US-11-056-355B-84957	Sequence 84957, A
459	67.5	4.8	801	6	US-10-471-571A-258	Sequence 258, App	532	67	4.8	552	6	US-11-056-355B-25184	Sequence 25184, A
460	67.5	4.8	939	7	US-11-056-355B-37226	Sequence 37226, A	533	67	4.8	555	7	US-11-056-355B-78306	Sequence 78306, A
461	67.5	4.8	939	7	US-11-056-355B-47979	Sequence 47979, A	534	67	4.8	559	6	US-10-953-349-11574	Sequence 11574, A
462	67.5	4.8	959	7	US-11-056-355B-48217	Sequence 48217, A	535	67	4.8	559	7	US-11-056-355B-48901	Sequence 48901, A
463	67.5	4.8	1054	7	US-11-056-355B-37225	Sequence 37225, A	536	67	4.8	567	7	US-11-056-355B-78305	Sequence 78305, A

537	67	4.8	602	7	US-11-056-355B-78059	Sequence 78059, A	610	66	4.7	320	7	US-11-226-554-139	Sequence 139, App
538	67	4.8	626	7	US-11-056-355B-38198	Sequence 38198, A	611	66	4.7	320	7	US-11-248-718-139	Sequence 139, App
539	67	4.8	626	7	US-11-056-355B-77180	Sequence 77180, A	612	66	4.7	350	6	US-10-449-902-53738	Sequence 53738, A
540	67	4.8	626	7	US-11-056-355B-104394	Sequence 104394, A	613	66	4.7	360	6	US-10-449-902-53506	Sequence 53506, A
541	67	4.8	626	7	US-11-056-355B-115633	Sequence 115633, A	614	66	4.7	368	6	US-10-449-902-47641	Sequence 47641, A
542	67	4.8	644	7	US-11-056-355B-38197	Sequence 38197, A	615	66	4.7	390	6	US-10-471-571A-2582	Sequence 2582, Ap
543	67	4.8	644	7	US-11-056-355B-77179	Sequence 77179, A	616	66	4.7	402	6	US-11-330-403-860	Sequence 860, App
544	67	4.8	644	7	US-11-056-355B-104393	Sequence 104393, A	617	66	4.7	432	6	US-10-471-571A-822	Sequence 822, App
545	67	4.8	644	7	US-11-056-355B-115632	Sequence 115632, A	618	66	4.7	432	6	US-10-449-902-31378	Sequence 31378, A
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547	67	4.8	674	7	US-11-330-403-12193	Sequence 12193, A	620	66	4.7	460	6	US-10-953-349-5285	Sequence 5285, Ap
548	67	4.8	695	7	US-11-056-355B-38196	Sequence 38196, A	621	66	4.7	460	7	US-11-330-403-10226	Sequence 10226, A
549	67	4.8	695	7	US-11-056-355B-77178	Sequence 77178, A	622	66	4.7	462	6	US-10-953-349-5284	Sequence 5284, Ap
550	67	4.8	695	7	US-11-056-355B-104392	Sequence 104392, A	623	66	4.7	471	7	US-11-056-355B-53655	Sequence 53655, A
551	67	4.8	695	7	US-11-056-355B-115631	Sequence 115631, A	624	66	4.7	513	6	US-10-953-349-5283	Sequence 5283, Ap
552	67	4.8	742	7	US-11-056-355B-78304	Sequence 78304, A	625	66	4.7	624	6	US-10-449-902-40952	Sequence 40952, A
553	67	4.8	967	6	US-10-505-405-2	Sequence 2, Appli	626	66	4.7	646	7	US-11-021-837-58	Sequence 58, Appl
554	67	4.8	967	6	US-10-505-405-6	Sequence 6, Appli	627	66	4.7	666	7	US-11-056-355B-72327	Sequence 72327, A
555	67	4.8	1332	7	US-11-301-094-6	Sequence 6, Appli	628	66	4.7	694	7	US-11-056-355B-71616	Sequence 71616, A
556	67	4.8	1359	7	US-11-270-796-22	Sequence 22, Appl	629	66	4.7	695	7	US-11-330-403-13159	Sequence 13159, A
557	66.5	4.8	241	7	US-11-347-766-18	Sequence 18, Appl	630	66	4.7	741	7	US-11-056-355B-72326	Sequence 72326, A
558	66.5	4.8	242	7	US-11-056-355B-1540	Sequence 1540, Ap	631	66	4.7	769	7	US-11-056-355B-71615	Sequence 71615, A
559	66.5	4.8	263	6	US-10-449-902-39161	Sequence 39161, A	632	66	4.7	790	6	US-10-449-902-52717	Sequence 52717, A
560	66.5	4.8	270	6	US-10-449-902-34690	Sequence 34690, A	633	66	4.7	853	7	US-11-056-355B-72325	Sequence 72325, A
561	66.5	4.8	287	6	US-10-471-571A-4460	Sequence 4460, Ap	634	66	4.7	881	7	US-11-056-355B-71614	Sequence 71614, A
562	66.5	4.8	297	7	US-11-330-403-6313	Sequence 6313, Ap	635	66	4.7	1333	7	US-11-270-796-3	Sequence 3, Appli
563	66.5	4.8	302	7	US-11-056-355B-1539	Sequence 1539, Ap	636	65.5	4.7	137	6	US-10-449-902-52012	Sequence 52012, A
564	66.5	4.8	310	7	US-11-056-355B-1538	Sequence 1538, Ap	637	65.5	4.7	186	6	US-10-449-902-31572	Sequence 31572, A
565	66.5	4.8	370	6	US-10-449-902-56226	Sequence 56226, A	638	65.5	4.7	194	6	US-10-449-902-43714	Sequence 43714, A
566	66.5	4.8	378	7	US-11-056-355B-3915	Sequence 3915, Ap	639	65.5	4.7	237	7	US-11-103-233-65	Sequence 65, Appl
567	66.5	4.8	391	6	US-10-953-349-21132	Sequence 21132, A	640	65.5	4.7	242	6	US-10-449-902-44536	Sequence 44536, A
568	66.5	4.8	396	7	US-11-056-355B-3914	Sequence 3914, Ap	641	65.5	4.7	286	7	US-11-056-355B-28777	Sequence 28777, A
569	66.5	4.8	408	6	US-10-953-349-21130	Sequence 21130, A	642	65.5	4.7	300	6	US-10-449-902-32367	Sequence 32367, A
570	66.5	4.8	428	6	US-10-953-349-21131	Sequence 21131, A	643	65.5	4.7	317	7	US-11-056-355B-70623	Sequence 70623, A
571	66.5	4.8	499	6	US-10-471-571A-3194	Sequence 3194, Ap	644	65.5	4.7	307	7	US-11-056-355B-70622	Sequence 70622, A
572	66.5	4.8	512	7	US-11-330-403-5812	Sequence 5812, Ap	645	65.5	4.7	311	7	US-11-056-355B-70621	Sequence 70621, A
573	66.5	4.8	513	7	US-11-330-403-8839	Sequence 8839, Ap	646	65.5	4.7	329	7	US-11-056-355B-69786	Sequence 69786, A
574	66.5	4.8	520	6	US-10-471-571A-5356	Sequence 5356, Ap	647	65.5	4.7	342	6	US-11-056-355B-69786	Sequence 69786, A
575	66.5	4.8	546	6	US-10-449-902-49911	Sequence 49911, A	648	65.5	4.7	352	6	US-10-449-902-35485	Sequence 35485, A
576	66.5	4.8	553	6	US-10-517-553-1	Sequence 1, Appli	649	65.5	4.7	355	6	US-10-516-032-8	Sequence 8, Appli
577	66.5	4.8	599	7	US-11-293-697-3454	Sequence 3454, Ap	650	65.5	4.7	360	6	US-10-449-902-36130	Sequence 36130, A
578	66.5	4.8	616	7	US-11-056-355B-100223	Sequence 100223, A	651	65.5	4.7	360	6	US-10-449-902-47417	Sequence 47417, A
579	66.5	4.8	616	7	US-11-056-355B-111462	Sequence 111462, A	652	65.5	4.7	367	7	US-11-056-355B-3278	Sequence 3278, Ap
580	66.5	4.8	661	6	US-10-449-902-33093	Sequence 33093, A	653	65.5	4.7	381	7	US-11-056-355B-19589	Sequence 19589, A
581	66.5	4.8	661	6	US-10-449-902-51012	Sequence 51012, A	654	65.5	4.7	383	7	US-11-056-355B-3277	Sequence 3277, Ap
582	66.5	4.8	685	7	US-11-056-355B-100222	Sequence 100222, A	655	65.5	4.7	390	7	US-11-056-355B-97731	Sequence 97731, A
583	66.5	4.8	685	7	US-11-056-355B-111461	Sequence 111461, A	656	65.5	4.7	390	7	US-11-056-355B-108970	Sequence 108970, A
584	66.5	4.8	696	6	US-10-539-228-574	Sequence 574, App	657	65.5	4.7	396	7	US-11-330-403-11889	Sequence 11889, A
585	66.5	4.8	717	7	US-11-056-355B-100221	Sequence 100221, A	658	65.5	4.7	397	7	US-11-330-403-4722	Sequence 4722, Ap
586	66.5	4.8	837	6	US-11-056-355B-111460	Sequence 111460, A	659	65.5	4.7	398	7	US-11-197-712-288	Sequence 288, App
587	66.5	4.8	899	7	US-10-449-902-45332	Sequence 45332, A	660	65.5	4.7	401	6	US-10-953-349-31569	Sequence 31569, A
588	66.5	4.8	941	6	US-11-377-884-48	Sequence 48, Appl	661	65.5	4.7	401	6	US-10-515-283A-5	Sequence 5, Appli
589	66.5	4.8	957	7	US-10-449-902-44419	Sequence 44419, A	662	65.5	4.7	401	7	US-11-264-737-54	Sequence 54, Appl
590	66.5	4.8	957	7	US-11-056-355B-79003	Sequence 79003, A	663	65.5	4.7	401	7	US-11-265-761-42	Sequence 42, Appl
591	66.5	4.8	960	7	US-11-256-173-15	Sequence 15, Appl	664	65.5	4.7	401	7	US-11-056-355B-66509	Sequence 66509, A
592	66.5	4.8	960	7	US-11-056-355B-70322	Sequence 70322, A	665	65.5	4.7	404	7	US-11-056-355B-19588	Sequence 19588, A
593	66.5	4.8	970	7	US-11-056-355B-79002	Sequence 79002, A	666	65.5	4.7	428	7	US-11-053-553-3	Sequence 3, Appli
594	66.5	4.8	973	7	US-11-056-355B-70321	Sequence 70321, A	667	65.5	4.7	431	7	US-11-330-403-12302	Sequence 12302, A
595	66.5	4.8	1085	7	US-11-056-355B-79001	Sequence 79001, A	668	65.5	4.7	463	6	US-10-953-349-31568	Sequence 31568, A
596	66.5	4.8	1088	7	US-11-056-355B-79001	Sequence 79001, A	669	65.5	4.7	463	7	US-11-056-355B-66508	Sequence 66508, A
597	66.5	4.8	1148	7	US-11-325-276-4	Sequence 4, Appli	670	65.5	4.7	464	7	US-11-330-403-3415	Sequence 3415, Ap
598	66.5	4.8	1704	7	US-11-289-102-341	Sequence 341, App	671	65.5	4.7	464	7	US-11-330-403-7852	Sequence 7852, Ap
599	66	4.7	285	7	US-11-056-355B-28819	Sequence 28819, A	672	65.5	4.7	464	7	US-11-330-403-10134	Sequence 10134, A
600	66	4.7	285	7	US-11-056-355B-32409	Sequence 32409, A	673	65.5	4.7	493	7	US-11-251-208-459	Sequence 459, App
601	66	4.7	285	7	US-11-056-355B-35822	Sequence 35822, A	674	65.5	4.7	494	7	US-11-330-403-18433	Sequence 18433, A
602	66	4.7	285	7	US-11-056-355B-85609	Sequence 85609, A	675	65.5	4.7	497	6	US-10-449-902-45839	Sequence 45839, A
603	66	4.7	285	7	US-11-056-355B-102377	Sequence 102377, A	676	65.5	4.7	517	6	US-10-471-571A-3562	Sequence 3562, Ap
604	66	4.7	285	7	US-11-056-355B-113616	Sequence 113616, A	677	65.5	4.7	654	6	US-10-471-571A-1262	Sequence 1262, Ap
605	66	4.7	290	7	US-11-330-403-15987	Sequence 15987, A	678	65.5	4.7	792	7	US-11-330-403-9551	Sequence 9551, Ap
606	66	4.7	298	7	US-11-056-355B-52855	Sequence 52855, A	679	65.5	4.7	799	6	US-10-449-902-53376	Sequence 53376, A
607	66	4.7	306	7	US-11-056-355B-35821	Sequence 35821, A	680	65.5	4.7	994	6	US-10-449-902-43721	Sequence 43721, A
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609	66	4.7	306	7	US-11-056-355B-113615	Sequence 113615, A	682	65.5	4.7	206	6	US-10-953-349-3843	Sequence 3843, Ap

683	65	4.7	206	7	US-11-056-355B-59163	Sequence 59163, A	756	64.5	4.6	343	6	US-10-540-898-807	Sequence 807, App
684	65	4.7	229	7	US-11-056-355B-22221	Sequence 22221, A	757	64.5	4.6	353	7	US-11-251-208-81	Sequence 81, Appl
685	65	4.7	248	7	US-11-056-355B-22221	Sequence 22221, A	758	64.5	4.6	355	7	US-11-056-355B-24739	Sequence 24739, A
686	65	4.7	251	6	US-10-953-349-3842	Sequence 2930, Ap	759	64.5	4.6	355	7	US-11-056-355B-106000	Sequence 106000, A
687	65	4.7	254	6	US-10-953-349-3841	Sequence 3841, Ap	760	64.5	4.6	355	7	US-11-056-355B-117239	Sequence 117239, A
688	65	4.7	263	7	US-11-056-355B-59162	Sequence 59162, Ap	761	64.5	4.6	361	7	US-11-056-355B-24738	Sequence 24738, A
689	65	4.7	265	7	US-11-056-355B-16166	Sequence 16166, A	762	64.5	4.6	361	7	US-11-056-355B-105999	Sequence 105999, A
690	65	4.7	271	7	US-11-056-355B-121205	Sequence 121205, A	763	64.5	4.6	361	7	US-11-056-355B-117238	Sequence 117238, A
691	65	4.7	276	7	US-11-056-355B-12903	Sequence 12903, A	764	64.5	4.6	366	6	US-10-953-349-38438	Sequence 38438, A
692	65	4.7	282	7	US-11-056-355B-8878	Sequence 8878, Ap	765	64.5	4.6	370	6	US-11-056-355B-24554	Sequence 24554, A
693	65	4.7	285	6	US-10-953-349-28002	Sequence 28002, A	766	64.5	4.6	370	6	US-10-953-349-4908	Sequence 4908, Ap
694	65	4.7	287	6	US-11-056-355B-83235	Sequence 83235, A	767	64.5	4.6	394	6	US-11-056-355B-6926	Sequence 6926, A
695	65	4.7	290	7	US-11-056-355B-105425	Sequence 105425, A	768	64.5	4.6	395	6	US-10-953-349-38437	Sequence 38437, A
696	65	4.7	291	7	US-11-056-355B-116664	Sequence 116664, A	769	64.5	4.6	401	7	US-11-056-355B-19198	Sequence 19198, A
697	65	4.7	302	7	US-11-056-355B-3724	Sequence 3724, Ap	770	64.5	4.6	421	7	US-11-056-355B-1202	Sequence 1202, Ap
698	65	4.7	308	7	US-11-056-355B-59161	Sequence 59161, A	771	64.5	4.6	426	7	US-11-056-355B-8	Sequence 8, Appl
699	65	4.7	319	7	US-11-056-355B-105424	Sequence 105424, A	772	64.5	4.6	429	7	US-11-056-355B-3369	Sequence 3369, Ap
700	65	4.7	319	7	US-11-056-355B-116663	Sequence 116663, A	773	64.5	4.6	438	6	US-10-449-902-53385	Sequence 53385, A
701	65	4.7	330	7	US-11-056-355B-83234	Sequence 83234, A	774	64.5	4.6	469	6	US-10-953-349-4907	Sequence 4907, Ap
702	65	4.7	332	6	US-10-471-571A-3224	Sequence 3224, Ap	775	64.5	4.6	472	7	US-11-056-355B-13903	Sequence 13903, A
703	65	4.7	354	6	US-10-953-349-3453	Sequence 3453, Ap	776	64.5	4.6	484	6	US-10-953-349-4906	Sequence 4906, Ap
704	65	4.7	354	7	US-11-056-355B-35815	Sequence 35815, A	777	64.5	4.6	501	7	US-11-056-355B-56971	Sequence 56971, A
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706	65	4.7	372	6	US-10-953-349-10674	Sequence 35814, A	779	64.5	4.6	513	6	US-10-471-571A-1992	Sequence 1992, Ap
707	65	4.7	372	7	US-11-056-355B-35814	Sequence 35814, A	780	64.5	4.6	548	6	US-10-449-902-47265	Sequence 47265, A
708	65	4.7	400	6	US-10-953-349-10675	Sequence 10675, A	781	64.5	4.6	604	7	US-11-056-355B-47707	Sequence 47707, A
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710	65	4.7	409	7	US-11-056-355B-49563	Sequence 49563, A	783	64.5	4.6	823	7	US-11-056-355B-2570	Sequence 2570, Ap
711	65	4.7	418	6	US-11-056-355B-37667	Sequence 37667, A	784	64.5	4.6	823	7	US-11-056-355B-5019	Sequence 5019, Ap
712	65	4.7	432	7	US-10-953-349-10674	Sequence 10674, A	785	64.5	4.6	823	7	US-11-056-355B-5025	Sequence 5025, Ap
713	65	4.7	418	7	US-11-056-355B-37668	Sequence 37668, A	786	64.5	4.6	823	7	US-11-056-355B-18196	Sequence 18196, A
714	65	4.7	418	7	US-11-056-355B-49562	Sequence 49562, A	787	64.5	4.6	823	7	US-11-056-355B-18196	Sequence 18196, A
715	65	4.7	418	7	US-11-056-355B-76798	Sequence 76798, A	788	64.5	4.6	2292	7	US-11-335-891-25	Sequence 25, Appl
716	65	4.7	432	6	US-10-953-349-10673	Sequence 10673, A	789	64	4.6	196	6	US-10-449-902-31753	Sequence 31753, A
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718	65	4.7	432	7	US-11-056-355B-49561	Sequence 49561, A	791	64	4.6	250	6	US-10-449-902-28625	Sequence 28625, A
719	65	4.7	432	7	US-11-056-355B-76797	Sequence 76797, A	792	64	4.6	250	6	US-10-449-902-30233	Sequence 30233, A
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721	65	4.7	451	7	US-11-056-355B-76796	Sequence 76796, A	794	64	4.6	268	7	US-11-056-355B-91496	Sequence 91496, A
722	65	4.7	458	7	US-11-226-908-8	Sequence 8, Appl	795	64	4.6	268	7	US-11-056-355B-91496	Sequence 91496, A
723	65	4.7	459	6	US-10-953-349-3451	Sequence 3451, Ap	796	64	4.6	278	6	US-11-056-355B-95252	Sequence 95252, A
724	65	4.7	459	7	US-11-056-355B-35813	Sequence 35813, A	797	64	4.6	278	6	US-10-953-349-24148	Sequence 24148, A
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726	65	4.7	462	7	US-11-226-908-6	Sequence 6, Appl	799	64	4.6	279	7	US-11-056-355B-91495	Sequence 91495, A
727	65	4.7	470	7	US-11-056-355B-70545	Sequence 70545, A	800	64	4.6	280	7	US-11-056-355B-95251	Sequence 95251, A
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729	65	4.7	500	7	US-11-056-355B-79327	Sequence 79327, A	802	64	4.6	281	7	US-11-056-355B-86636	Sequence 86636, A
730	65	4.7	518	6	US-10-196-749-72	Sequence 72, Appl	803	64	4.6	282	7	US-11-056-355B-86635	Sequence 86635, A
731	65	4.7	518	7	US-11-056-355B-97326	Sequence 97326, A	804	64	4.6	292	7	US-11-056-355B-1541	Sequence 1541, Ap
732	65	4.7	540	7	US-11-056-355B-711	Sequence 711, Ap	805	64	4.6	296	7	US-11-249-111-103	Sequence 103, App
733	65	4.7	555	7	US-11-056-355B-6828	Sequence 6828, Ap	806	64	4.6	296	7	US-11-056-355B-82159	Sequence 82159, A
734	65	4.7	581	7	US-11-251-465-18	Sequence 18, Appl	807	64	4.6	297	7	US-11-056-355B-82158	Sequence 82158, A
735	65	4.7	614	7	US-11-056-355B-8768	Sequence 8768, Ap	808	64	4.6	298	7	US-11-056-355B-82157	Sequence 82157, A
736	65	4.7	662	6	US-10-471-571A-5102	Sequence 5102, Ap	809	64	4.6	330	7	US-11-056-355B-13532	Sequence 13532, A
737	65	4.7	866	6	US-10-449-902-52724	Sequence 52724, A	810	64	4.6	334	6	US-11-056-355B-13532	Sequence 13532, A
738	64.5	4.6	195	6	US-10-953-349-37920	Sequence 37920, A	811	64	4.6	334	6	US-10-953-349-2782	Sequence 2782, A
739	64.5	4.6	211	6	US-10-953-349-37919	Sequence 37919, A	812	64	4.6	339	6	US-11-056-355B-64683	Sequence 64683, A
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741	64.5	4.6	286	7	US-11-056-355B-97694	Sequence 97694, A	814	64	4.6	357	6	US-10-471-571A-544	Sequence 5444, Ap
742	64.5	4.6	286	7	US-11-056-355B-108933	Sequence 108933, A	815	64	4.6	364	7	US-11-056-355B-13531	Sequence 13531, A
743	64.5	4.6	287	6	US-10-953-349-2977	Sequence 2977, Ap	816	64	4.6	366	6	US-10-953-349-17831	Sequence 17831, A
744	64.5	4.6	287	7	US-11-056-355B-26812	Sequence 26812, A	817	64	4.6	366	6	US-10-449-902-47698	Sequence 47698, A
745	64.5	4.6	287	7	US-11-056-355B-87735	Sequence 87735, A	818	64	4.6	366	6	US-10-449-902-47755	Sequence 47755, A
746	64.5	4.6	291	7	US-11-056-355B-5805	Sequence 5805, Ap	819	64	4.6	367	6	US-10-953-349-27781	Sequence 27781, A
747	64.5	4.6	323	6	US-10-953-349-38439	Sequence 38439, A	820	64	4.6	376	7	US-11-056-355B-64682	Sequence 64682, A
748	64.5	4.6	335	7	US-11-056-355B-106001	Sequence 106001, A	821	64	4.6	394	6	US-11-056-355B-13530	Sequence 13530, A
749	64.5	4.6	337	7	US-11-056-355B-106001	Sequence 106001, A	822	64	4.6	403	7	US-10-535-928A-41	Sequence 41, Appl
750	64.5	4.6	338	6	US-10-527-788-69	Sequence 69, Appl	823	64	4.6	409	7	US-11-197-712-249	Sequence 249, App
751	64.5	4.6	335	7	US-11-056-355B-24740	Sequence 24740, A	824	64	4.6	424	7	US-11-056-355B-11557	Sequence 11557, A
752	64.5	4.6	335	7	US-11-056-355B-106001	Sequence 106001, A	825	64	4.6	425	7	US-11-056-355B-57320	Sequence 57320, A
753	64.5	4.6	335	7	US-11-056-355B-117240	Sequence 117240, A	826	64	4.6	439	7	US-11-056-355B-57319	Sequence 57319, A
754	64.5	4.6	343	6	US-10-540-898-803	Sequence 803, App	827	64	4.6	439	7	US-11-056-355B-57319	Sequence 57319, A
755	64.5	4.6	343	6	US-10-540-898-805	Sequence 805, App	828	64	4.6	460	7	US-11-330-403-12867	Sequence 12867, A

829	64	4.6	487	6	US-10-953-349-10426	Sequence 10436, A	902	63.5	4.6	412	7	US-11-056-355B-74957	Sequence 74957, A
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831	64	4.6	487	7	US-11-056-355B-85105	Sequence 85105, A	904	63.5	4.6	424	7	US-11-056-355B-31214	Sequence 31214, A
832	64	4.6	490	7	US-11-330-403-1544	Sequence 1544, Ap	905	63.5	4.6	426	7	US-11-056-355B-27623	Sequence 27623, A
833	64	4.6	493	7	US-10-953-349-10425	Sequence 10425, A	906	63.5	4.6	426	7	US-11-056-355B-31213	Sequence 31213, A
834	64	4.6	493	7	US-11-056-355B-49280	Sequence 49280, A	907	63.5	4.6	434	7	US-11-174-307B-3666	Sequence 3666, Ap
835	64	4.6	493	7	US-11-056-355B-85104	Sequence 85104, A	908	63.5	4.6	435	7	US-11-296-657-72	Sequence 72, Appl
836	64	4.6	509	6	US-10-953-349-10424	Sequence 10424, A	909	63.5	4.6	435	7	US-11-056-355B-52482	Sequence 52482, A
837	64	4.6	509	7	US-11-056-355B-49279	Sequence 49279, A	910	63.5	4.6	441	6	US-10-449-902-40892	Sequence 40892, A
838	64	4.6	509	7	US-11-056-355B-85103	Sequence 85103, A	911	63.5	4.6	441	6	US-10-449-902-44009	Sequence 44009, A
839	64	4.6	509	7	US-11-330-403-18229	Sequence 18229, A	912	63.5	4.6	448	6	US-10-449-902-52836	Sequence 52836, A
840	64	4.6	520	7	US-11-330-403-9849	Sequence 9849, Ap	913	63.5	4.6	448	6	US-11-317-789A-7075	Sequence 7075, Ap
841	64	4.6	548	7	US-11-056-355B-57318	Sequence 57318, A	914	63.5	4.6	449	7	US-11-056-355B-74956	Sequence 74956, A
842	64	4.6	553	7	US-11-330-403-1906	Sequence 1906, Ap	915	63.5	4.6	449	7	US-11-056-355B-74956	Sequence 74956, A
843	64	4.6	578	6	US-11-330-403-15368	Sequence 15368, A	916	63.5	4.6	451	7	US-11-330-403-4120	Sequence 4120, Ap
844	64	4.6	586	6	US-10-449-902-39151	Sequence 39151, A	917	63.5	4.6	460	7	US-11-056-355B-40263	Sequence 40263, A
845	64	4.6	586	7	US-11-330-403-14209	Sequence 14209, A	918	63.5	4.6	460	7	US-11-056-355B-70724	Sequence 70724, A
846	64	4.6	618	7	US-11-330-403-7153	Sequence 7153, Ap	919	63.5	4.6	460	7	US-11-056-355B-74955	Sequence 74955, A
847	64	4.6	658	7	US-11-174-307B-3680	Sequence 3680, Ap	920	63.5	4.6	488	7	US-11-242-505A-30	Sequence 30, Appl
848	64	4.6	664	7	US-11-056-355B-46978	Sequence 46978, A	921	63.5	4.6	488	7	US-11-404-939-561	Sequence 561, App
849	64	4.6	666	6	US-10-953-349-3549	Sequence 3549, Ap	922	63.5	4.6	510	7	US-11-330-403-15785	Sequence 15785, A
850	64	4.6	673	7	US-11-056-355B-46977	Sequence 46977, A	923	63.5	4.6	605	7	US-11-330-403-4015	Sequence 4015, Ap
851	64	4.6	682	6	US-10-449-902-36546	Sequence 36546, A	924	63.5	4.6	787	6	US-10-449-902-43812	Sequence 43812, A
852	64	4.6	682	6	US-10-449-902-36546	Sequence 36546, A	925	63.5	4.6	2292	7	US-11-335-891-26	Sequence 26, Appl
853	64	4.6	690	6	US-10-953-349-3548	Sequence 3548, Ap	926	63.5	4.6	2292	7	US-11-335-891-28	Sequence 28, Appl
854	64	4.6	807	6	US-10-449-902-44460	Sequence 44460, A	927	63	4.5	185	6	US-10-953-349-15254	Sequence 15254, A
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856	64	4.6	875	7	US-11-056-355B-75347	Sequence 75347, A	929	63	4.5	238	6	US-10-449-902-30619	Sequence 30619, A
857	64	4.6	891	7	US-11-056-355B-73566	Sequence 73566, A	930	63	4.5	238	6	US-10-449-902-31961	Sequence 31961, A
858	64	4.6	902	6	US-10-953-349-3547	Sequence 3547, Ap	931	63	4.5	238	6	US-10-449-902-48149	Sequence 48149, A
859	64	4.6	919	7	US-11-056-355B-75346	Sequence 75346, A	932	63	4.5	247	6	US-10-953-349-15253	Sequence 15253, A
860	64	4.6	926	7	US-11-056-355B-73565	Sequence 73565, A	933	63	4.5	247	6	US-10-953-349-37011	Sequence 37011, A
861	64	4.6	954	7	US-11-056-355B-75345	Sequence 75345, A	934	63	4.5	247	7	US-11-056-355B-55918	Sequence 55918, A
862	64	4.6	1488	7	US-11-330-403-15631	Sequence 15631, A	935	63	4.5	259	6	US-10-522-356-22	Sequence 22, Appl
863	64	4.6	1551	7	US-11-377-884-46	Sequence 46, Appl	936	63	4.5	271	6	US-10-953-349-23075	Sequence 23075, A
864	64	4.6	2301	7	US-11-335-891-30	Sequence 30, Appl	937	63	4.5	280	6	US-10-953-349-23074	Sequence 23074, A
865	63.5	4.6	132	6	US-10-449-902-36004	Sequence 36004, A	938	63	4.5	297	6	US-11-355-735-2	Sequence 2, Appl1
866	63.5	4.6	218	6	US-10-504-973-24	Sequence 24, Appl	939	63	4.5	290	7	US-11-340-429-4	Sequence 4, Appl1
867	63.5	4.6	269	6	US-10-471-571A-4828	Sequence 4828, Ap	940	63	4.5	290	7	US-11-378-707-14	Sequence 14, Appl
868	63.5	4.6	269	6	US-10-449-902-48668	Sequence 48668, A	941	63	4.5	293	7	US-11-346-468-2	Sequence 2, Appl1
869	63.5	4.6	273	7	US-11-056-355B-45627	Sequence 45627, A	942	63	4.5	293	7	US-11-330-403-7498	Sequence 7498, Ap
870	63.5	4.6	273	7	US-11-056-355B-50569	Sequence 50569, A	943	63	4.5	299	6	US-10-953-349-15252	Sequence 15252, A
871	63.5	4.6	280	6	US-10-953-349-27087	Sequence 27087, A	944	63	4.5	299	7	US-11-056-355B-55917	Sequence 55917, A
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873	63.5	4.6	284	6	US-10-953-349-27086	Sequence 27086, A	946	63	4.5	333	7	US-11-056-355B-84881	Sequence 84881, A
874	63.5	4.6	284	6	US-11-056-355B-62841	Sequence 62841, A	947	63	4.5	350	7	US-11-056-355B-84880	Sequence 84880, A
875	63.5	4.6	286	6	US-10-953-349-9374	Sequence 9374, Ap	948	63	4.5	358	7	US-11-056-355B-84879	Sequence 84879, A
876	63.5	4.6	286	7	US-11-056-355B-25360	Sequence 25360, A	949	63	4.5	364	7	US-11-293-697-4612	Sequence 4612, Ap
877	63.5	4.6	288	7	US-11-330-403-15256	Sequence 15256, A	950	63	4.5	397	6	US-10-471-571A-5338	Sequence 5338, Ap
878	63.5	4.6	289	7	US-11-056-355B-25394	Sequence 25394, Ap	951	63	4.5	410	6	US-11-174-307B-3942	Sequence 3942, Ap
879	63.5	4.6	295	6	US-10-953-349-23478	Sequence 23478, A	952	63	4.5	413	6	US-10-953-349-38771	Sequence 38771, A
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881	63.5	4.6	315	7	US-11-056-355B-27625	Sequence 27625, A	954	63	4.5	416	6	US-10-449-902-47396	Sequence 47396, A
882	63.5	4.6	315	7	US-11-056-355B-31215	Sequence 31215, A	955	63	4.5	418	6	US-10-953-349-23073	Sequence 23073, A
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884	63.5	4.6	348	6	US-10-953-349-23477	Sequence 23477, A	957	63	4.5	462	6	US-10-953-349-38769	Sequence 38769, A
885	63.5	4.6	353	7	US-11-264-784-63	Sequence 63, Appl	958	63	4.5	463	6	US-10-449-902-53826	Sequence 53826, A
886	63.5	4.6	353	7	US-11-264-737-96	Sequence 96, Appl	959	63	4.5	486	6	US-10-449-902-43179	Sequence 43179, A
887	63.5	4.6	353	7	US-11-265-761-76	Sequence 76, Appl	960	63	4.5	486	7	US-11-330-403-6277	Sequence 6277, Ap
888	63.5	4.6	354	6	US-10-953-349-23476	Sequence 23476, A	961	63	4.5	498	7	US-11-330-403-2313	Sequence 2313, Ap
889	63.5	4.6	356	7	US-11-384-847-7	Sequence 7, Appl1	962	63	4.5	512	6	US-10-471-571A-2270	Sequence 2270, Ap
890	63.5	4.6	357	6	US-10-953-349-23681	Sequence 23681, A	963	63	4.5	527	6	US-10-539-228-787	Sequence 787, App
891	63.5	4.6	358	7	US-11-330-403-10791	Sequence 10791, A	964	63	4.5	530	7	US-11-296-657-10	Sequence 10, Appl
892	63.5	4.6	374	6	US-10-953-349-23680	Sequence 23680, A	965	63	4.5	539	7	US-11-330-403-12434	Sequence 12434, A
893	63.5	4.6	374	6	US-11-330-403-10227	Sequence 10227, A	966	63	4.5	576	6	US-10-449-902-52631	Sequence 52631, A
894	63.5	4.6	375	6	US-10-953-349-23679	Sequence 23679, A	967	63	4.5	590	6	US-10-449-902-45694	Sequence 45694, A
895	63.5	4.6	394	6	US-11-330-403-2843	Sequence 2843, Ap	968	63	4.5	590	6	US-10-449-902-49011	Sequence 49011, A
896	63.5	4.6	402	6	US-10-449-902-47229	Sequence 47229, A	969	63	4.5	610	7	US-11-330-403-16759	Sequence 16759, A
897	63.5	4.6	403	6	US-10-449-902-55879	Sequence 55879, A	970	63	4.5	658	6	US-10-953-349-4215	Sequence 4215, Ap
898	63.5	4.6	403	6	US-10-471-571A-2620	Sequence 2620, Ap	971	63	4.5	660	6	US-10-953-349-4214	Sequence 4214, Ap
899	63.5	4.6	411	7	US-11-056-355B-40265	Sequence 40265, A	972	63	4.5	661	6	US-10-953-349-4213	Sequence 4213, Ap
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901	63.5	4.6	412	7	US-11-056-355B-70726	Sequence 70726, A	974	63	4.5	691	7	US-11-056-355B-48027	Sequence 48027, A

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977	63	4.5	697	7	US-11-056-355B-48026	Sequence 48026, A	1050	62.5	4.5	583	7	US-11-330-403-18668	Sequence 18668, A
978	63	4.5	735	7	US-11-293-697-4426	Sequence 4426, Ap	1051	62.5	4.5	587	7	US-11-292-951-4	Sequence 4, Appli
979	63	4.5	772	7	US-11-056-355B-44817	Sequence 44817, A	1052	62.5	4.5	595	6	US-10-517-352-9	Sequence 9, Appli
980	63	4.5	772	7	US-11-056-355B-48025	Sequence 48025, A	1053	62.5	4.5	595	6	US-10-517-420-35	Sequence 35, Appli
981	63	4.5	777	7	US-11-330-403-10510	Sequence 10510, A	1054	62.5	4.5	597	7	US-11-330-403-15178	Sequence 15178, A
982	63	4.5	822	7	US-11-330-403-7212	Sequence 7212, Ap	1055	62.5	4.5	616	7	US-11-056-355B-86327	Sequence 86327, A
983	63	4.5	822	7	US-11-330-403-17883	Sequence 17883, A	1056	62.5	4.5	632	7	US-11-056-355B-72810	Sequence 72810, A
984	63	4.5	828	7	US-11-330-403-12723	Sequence 12723, A	1057	62.5	4.5	640	6	US-10-953-349-24506	Sequence 24506, A
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986	63	4.5	1016	6	US-10-449-902-45738	Sequence 45738, A	1059	62.5	4.5	644	6	US-10-517-420-47	Sequence 47, Appl
987	63	4.5	1215	6	US-10-953-349-8001	Sequence 8001, Ap	1060	62.5	4.5	652	6	US-10-517-420-27	Sequence 27, Appl
988	63	4.5	1215	7	US-11-056-355B-39533	Sequence 39533, A	1061	62.5	4.5	652	6	US-10-517-420-41	Sequence 41, Appl
989	63	4.5	1215	7	US-11-056-355B-106299	Sequence 106299, A	1062	62.5	4.5	659	7	US-11-056-355B-81954	Sequence 81954, A
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992	63	4.5	1355	7	US-11-056-355B-39532	Sequence 39532, A	1065	62.5	4.5	694	6	US-10-517-420-46	Sequence 46, Appl
993	63	4.5	1355	7	US-11-056-355B-106298	Sequence 106298, A	1066	62.5	4.5	694	6	US-10-517-420-47	Sequence 47, Appl
994	63	4.5	1355	7	US-11-056-355B-117537	Sequence 117537, A	1067	62.5	4.5	694	6	US-10-517-420-48	Sequence 48, Appl
995	63	4.5	1514	6	US-10-953-349-7999	Sequence 7999, Ap	1068	62.5	4.5	698	6	US-10-953-349-4543	Sequence 4543, Ap
996	63	4.5	1514	7	US-11-133-075-9	Sequence 9, Appli	1069	62.5	4.5	709	6	US-10-953-349-4542	Sequence 4542, Ap
997	63	4.5	1514	7	US-11-056-355B-39531	Sequence 39531, A	1070	62.5	4.5	725	6	US-10-953-349-4541	Sequence 4541, Ap
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1002	62.5	4.5	255	7	US-11-319-952-75	Sequence 75, Appli	1075	62.5	4.5	995	6	US-10-471-571A-3910	Sequence 3910, Ap
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1005	62.5	4.5	286	6	US-10-449-902-50826	Sequence 50826, A	1078	62.5	4.5	1165	7	US-11-325-276-8	Sequence 8, Appli
1006	62.5	4.5	289	6	US-10-449-902-32900	Sequence 32900, A	1079	62.5	4.5	2516	7	US-11-070-573-25	Sequence 25, Appl
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1008	62.5	4.5	306	7	US-11-174-307B-2978	Sequence 2978, Ap	1081	62	4.5	189	7	US-11-056-355B-95803	Sequence 95803, A
1009	62.5	4.5	323	6	US-10-449-902-30512	Sequence 30512, A	1082	62	4.5	202	6	US-10-374-780A-2878	Sequence 2878, Ap
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1012	62.5	4.5	332	7	US-11-297-134-48	Sequence 48, Appl	1085	62	4.5	203	7	US-11-056-355B-9906	Sequence 9906, Ap
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1014	62.5	4.5	336	7	US-11-174-307B-4360	Sequence 4360, Ap	1087	62	4.5	279	7	US-11-056-355B-87147	Sequence 87147, A
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1018	62.5	4.5	401	7	US-11-056-355B-71016	Sequence 71016, A	1091	62	4.5	292	7	US-11-330-403-14906	Sequence 14906, A
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1024	62.5	4.5	494	7	US-11-330-403-5699	Sequence 5699, Ap	1097	62	4.5	328	6	US-10-527-788-53	Sequence 53, Appl
1025	62.5	4.5	504	6	US-10-539-228-334	Sequence 334, App	1098	62	4.5	331	6	US-10-449-902-50702	Sequence 50702, A
1026	62.5	4.5	504	6	US-10-539-228-336	Sequence 336, App	1099	62	4.5	331	7	US-11-056-355B-64841	Sequence 64841, A
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1030	62.5	4.5	507	7	US-11-056-355B-38166	Sequence 38166, A	1103	62	4.5	354	7	US-11-056-355B-84522	Sequence 84522, A
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1033	62.5	4.5	514	7	US-11-056-355B-72811	Sequence 72811, A	1106	62	4.5	357	7	US-11-056-355B-100468	Sequence 100468, A
1034	62.5	4.5	523	6	US-10-953-349-2275	Sequence 2275, Ap	1107	62	4.5	357	7	US-11-056-355B-111707	Sequence 111707, A
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1038	62.5	4.5	525	7	US-11-330-403-6781	Sequence 6781, Ap	1111	62	4.5	363	6	US-10-544-615-2	Sequence 2, Appli
1039	62.5	4.5	535	7	US-11-174-307B-3218	Sequence 3218, Ap	1112	62	4.5	363	6	US-10-530-902-2	Sequence 2, Appli
1040	62.5	4.5	535	7	US-11-330-403-14467	Sequence 14467, A	1113	62	4.5	363	7	US-11-056-355B-40833	Sequence 40833, A
1041	62.5	4.5	553	6	US-10-517-552-5	Sequence 5, Appli	1114	62	4.5	363	7	US-11-056-355B-100467	Sequence 100467, A
1042	62.5	4.5	553	6	US-10-517-552-5	Sequence 5, Appli	1115	62	4.5	363	7	US-11-056-355B-111706	Sequence 111706, A
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1044	62.5	4.5	553	7	US-11-226-554-99	Sequence 99, Appl	1117	62	4.5	368	7	US-11-056-355B-84521	Sequence 84521, A
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1047	62.5	4.5	570	7	US-11-056-355B-40911	Sequence 40911, A	1120	62	4.5	387	7	US-11-377-517-2	Sequence 2, Appli

1121	62	4.5	388	7	US-11-056-355B-36001	Sequence 36001, A	1194	62	4.5	884	6	US-10-449-902-41592	Sequence 41592, A
1122	62	4.5	390	6	US-10-953-349-4812	Sequence 4812, Ap	1195	62	4.5	980	7	US-11-242-505A-36	Sequence 36, Appl
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1125	62	4.5	390	7	US-11-056-355B-100466	Sequence 100466, A	1198	62	4.5	1233	7	US-11-056-355B-83993	Sequence 83993, A
1126	62	4.5	390	7	US-11-056-355B-111705	Sequence 111705, A	1199	62	4.5	1256	6	US-10-511-937-2975	Sequence 2975, Ap
1127	62	4.5	399	7	US-11-056-355B-80869	Sequence 80869, A	1200	62	4.5	1263	7	US-11-056-355B-83992	Sequence 83992, A
1128	62	4.5	400	7	US-11-056-355B-87146	Sequence 87146, A	1201	62	4.5	2227	7	US-11-409-670-12	Sequence 12, Appl
1129	62	4.5	402	7	US-11-330-403-7592	Sequence 7592, Ap	1202	62	4.5	2227	7	US-11-411-493-12	Sequence 12, Appl
1130	62	4.5	406	7	US-11-056-355B-35999	Sequence 35999, Ap	1203	61.5	4.4	135	7	US-11-056-355B-11088	Sequence 11088, A
1131	62	4.5	410	7	US-11-293-697-3074	Sequence 3074, Ap	1204	61.5	4.4	140	7	US-11-056-355B-11087	Sequence 11087, A
1132	62	4.5	412	7	US-11-330-403-3157	Sequence 3157, Ap	1205	61.5	4.4	167	7	US-11-056-355B-75507	Sequence 75507, A
1133	62	4.5	415	7	US-11-056-355B-64839	Sequence 64839, A	1206	61.5	4.4	168	7	US-11-122-986-176	Sequence 176, App
1134	62	4.5	427	7	US-11-056-355B-87145	Sequence 87145, A	1207	61.5	4.4	168	7	US-11-122-986-178	Sequence 178, App
1135	62	4.5	427	7	US-11-056-355B-102003	Sequence 102003, A	1208	61.5	4.4	190	6	US-10-953-349-34819	Sequence 34819, A
1136	62	4.5	432	7	US-11-056-355B-113242	Sequence 113242, A	1209	61.5	4.4	190	7	US-11-056-355B-8413	Sequence 8413, Ap
1137	62	4.5	436	6	US-10-953-349-33360	Sequence 33360, A	1210	61.5	4.4	226	6	US-10-953-349-26861	Sequence 26861, A
1138	62	4.5	436	7	US-11-056-355B-67493	Sequence 67493, A	1211	61.5	4.4	226	6	US-11-056-355B-68803	Sequence 68803, A
1139	62	4.5	440	7	US-11-056-355B-80868	Sequence 80868, A	1212	61.5	4.4	231	6	US-10-953-349-34818	Sequence 34818, A
1140	62	4.5	443	6	US-10-953-349-1222	Sequence 1222, Ap	1213	61.5	4.4	231	7	US-11-056-355B-8412	Sequence 8412, Ap
1141	62	4.5	443	7	US-11-056-355B-37910	Sequence 37910, A	1214	61.5	4.4	252	7	US-11-330-403-7361	Sequence 7361, Ap
1142	62	4.5	443	7	US-11-056-355B-104208	Sequence 104208, A	1215	61.5	4.4	252	6	US-10-449-902-32147	Sequence 32147, A
1143	62	4.5	443	7	US-11-056-355B-115447	Sequence 115447, A	1216	61.5	4.4	266	6	US-10-449-902-32787	Sequence 32787, A
1144	62	4.5	451	7	US-11-056-355B-102002	Sequence 102002, A	1217	61.5	4.4	266	6	US-10-449-902-34901	Sequence 34901, A
1145	62	4.5	451	7	US-11-056-355B-113241	Sequence 113241, A	1218	61.5	4.4	266	6	US-10-449-902-48576	Sequence 48576, A
1146	62	4.5	452	6	US-10-953-349-33259	Sequence 33259, A	1219	61.5	4.4	271	6	US-10-953-349-26860	Sequence 26860, A
1147	62	4.5	452	7	US-11-056-355B-67492	Sequence 67492, A	1220	61.5	4.4	271	7	US-11-056-355B-68802	Sequence 68802, A
1148	62	4.5	459	6	US-11-330-403-13256	Sequence 13256, A	1221	61.5	4.4	283	7	US-11-330-403-10306	Sequence 10306, A
1149	62	4.5	462	6	US-10-953-349-1221	Sequence 1221, Ap	1222	61.5	4.4	284	7	US-11-056-355B-40430	Sequence 40430, A
1150	62	4.5	462	6	US-10-449-902-42630	Sequence 42630, A	1223	61.5	4.4	286	6	US-10-953-349-9378	Sequence 9378, Ap
1151	62	4.5	462	7	US-11-056-355B-37909	Sequence 37909, A	1224	61.5	4.4	286	7	US-11-056-355B-21562	Sequence 21562, A
1152	62	4.5	462	7	US-11-056-355B-104207	Sequence 104207, A	1225	61.5	4.4	286	7	US-11-056-355B-27566	Sequence 27566, A
1153	62	4.5	462	7	US-11-056-355B-115446	Sequence 115446, A	1226	61.5	4.4	286	7	US-11-056-355B-31156	Sequence 31156, A
1154	62	4.5	468	7	US-11-056-355B-104206	Sequence 104206, A	1227	61.5	4.4	286	7	US-11-056-355B-97671	Sequence 97671, A
1155	62	4.5	468	7	US-11-056-355B-115445	Sequence 115445, A	1228	61.5	4.4	286	7	US-11-056-355B-107306	Sequence 107306, A
1156	62	4.5	469	6	US-10-953-349-1220	Sequence 1220, Ap	1229	61.5	4.4	286	7	US-11-056-355B-108910	Sequence 108910, A
1157	62	4.5	469	7	US-11-056-355B-37908	Sequence 37908, A	1230	61.5	4.4	286	7	US-11-056-355B-118545	Sequence 118545, A
1158	62	4.5	473	6	US-10-449-902-37398	Sequence 37398, A	1231	61.5	4.4	287	6	US-10-471-571A-2504	Sequence 2504, Ap
1159	62	4.5	473	7	US-11-330-403-18000	Sequence 18000, A	1232	61.5	4.4	287	7	US-11-366-001-55	Sequence 55, Appl
1160	62	4.5	475	6	US-11-056-355B-81356	Sequence 81356, A	1233	61.5	4.4	295	7	US-11-330-403-1368	Sequence 1368, Ap
1161	62	4.5	490	6	US-10-953-349-33358	Sequence 33358, A	1234	61.5	4.4	297	7	US-11-257-851A-73	Sequence 73, Appl
1162	62	4.5	490	7	US-11-056-355B-67491	Sequence 67491, A	1235	61.5	4.4	298	6	US-10-953-349-34817	Sequence 34817, A
1163	62	4.5	497	7	US-11-330-403-3469	Sequence 3469, Ap	1236	61.5	4.4	298	7	US-11-056-355B-8411	Sequence 8411, Ap
1164	62	4.5	498	7	US-11-056-355B-80867	Sequence 80867, A	1237	61.5	4.4	300	7	US-11-330-403-209	Sequence 209, App
1165	62	4.5	514	7	US-11-330-403-18670	Sequence 18670, A	1238	61.5	4.4	322	6	US-10-953-349-26859	Sequence 26859, A
1166	62	4.5	518	7	US-11-330-403-10672	Sequence 10672, Ap	1239	61.5	4.4	322	7	US-11-056-355B-68801	Sequence 68801, A
1167	62	4.5	528	7	US-11-330-403-8273	Sequence 8273, Ap	1240	61.5	4.4	323	6	US-10-449-902-31834	Sequence 31834, A
1168	62	4.5	528	7	US-11-330-403-13242	Sequence 13242, A	1241	61.5	4.4	341	7	US-11-056-355B-106029	Sequence 106029, A
1169	62	4.5	533	7	US-11-330-403-5636	Sequence 5636, Ap	1242	61.5	4.4	341	7	US-11-056-355B-117268	Sequence 117268, A
1170	62	4.5	548	6	US-10-449-902-52715	Sequence 52715, A	1243	61.5	4.4	358	7	US-11-024-544A-126	Sequence 126, App
1171	62	4.5	557	7	US-11-330-403-2683	Sequence 2683, Ap	1244	61.5	4.4	358	7	US-11-024-545-54	Sequence 54, Appl
1172	62	4.5	562	7	US-11-056-355B-70108	Sequence 70108, A	1245	61.5	4.4	358	7	US-11-190-750-109	Sequence 109, App
1173	62	4.5	570	7	US-11-056-355B-70107	Sequence 70107, A	1246	61.5	4.4	358	7	US-11-251-466-28	Sequence 28, Appl
1174	62	4.5	572	7	US-11-330-403-2118	Sequence 2118, Ap	1247	61.5	4.4	358	7	US-11-254-173-44	Sequence 44, Appl
1175	62	4.5	574	6	US-10-953-349-12942	Sequence 12942, A	1248	61.5	4.4	358	7	US-11-264-784-15	Sequence 15, Appl
1176	62	4.5	585	6	US-10-449-902-55150	Sequence 55150, A	1249	61.5	4.4	358	7	US-11-264-737-20	Sequence 20, Appl
1177	62	4.5	586	6	US-11-330-403-4419	Sequence 4419, Ap	1250	61.5	4.4	358	7	US-11-265-761-15	Sequence 15, Appl
1178	62	4.5	619	6	US-10-449-902-53242	Sequence 53242, A	1251	61.5	4.4	358	7	US-11-056-355B-106028	Sequence 106028, A
1179	62	4.5	633	6	US-10-471-571A-1140	Sequence 1140, Ap	1252	61.5	4.4	358	7	US-11-056-355B-117267	Sequence 117267, A
1180	62	4.5	633	7	US-11-056-355B-90909	Sequence 90909, A	1253	61.5	4.4	361	7	US-11-056-355B-106027	Sequence 106027, A
1181	62	4.5	633	7	US-11-056-355B-94665	Sequence 94665, A	1254	61.5	4.4	361	7	US-11-056-355B-117266	Sequence 117266, A
1182	62	4.5	636	6	US-10-953-349-12941	Sequence 12941, A	1255	61.5	4.4	366	6	US-10-471-571A-4838	Sequence 4838, Ap
1183	62	4.5	638	6	US-10-953-349-12940	Sequence 12940, A	1256	61.5	4.4	377	7	US-11-330-403-7801	Sequence 7801, Ap
1184	62	4.5	644	6	US-10-471-571A-4096	Sequence 4096, Ap	1257	61.5	4.4	406	7	US-11-330-403-8235	Sequence 8235, Ap
1185	62	4.5	653	7	US-11-056-355B-90908	Sequence 90908, A	1258	61.5	4.4	407	7	US-11-330-403-1358	Sequence 1358, Ap
1186	62	4.5	653	7	US-11-056-355B-94664	Sequence 94664, A	1259	61.5	4.4	423	7	US-11-330-403-3337	Sequence 3337, Ap
1187	62	4.5	673	7	US-11-056-355B-90907	Sequence 90907, A	1260	61.5	4.4	425	7	US-11-330-403-15364	Sequence 15364, A
1188	62	4.5	673	7	US-11-056-355B-94663	Sequence 94663, A	1261	61.5	4.4	426	7	US-11-178-538-45	Sequence 45, Appl
1189	62	4.5	744	6	US-11-330-403-6236	Sequence 6236, Ap	1262	61.5	4.4	441	7	US-11-056-355B-106721	Sequence 106721, A
1190	62	4.5	770	6	US-10-449-902-43017	Sequence 43017, A	1263	61.5	4.4	441	7	US-11-056-355B-117960	Sequence 117960, A
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1192	62	4.5	851	6	US-10-449-902-43432	Sequence 43432, A	1265	61.5	4.4	445	7	US-11-404-939-451	Sequence 451, App
1193	62	4.5	884	6	US-10-449-902-41313	Sequence 41313, A	1266	61.5	4.4	449	6	US-10-449-902-53110	Sequence 53110, A

1267	61.5	4.4	4.4	6	US-10-953-349-2648	Sequence 2648, Ap	1340	61	4.4	336	6	US-10-471-571A-510	Sequence 510, App
1268	61.5	4.4	4.4	465	US-10-449-902-52165	Sequence 52165, A	1341	61	4.4	344	7	US-11-056-355B-8179	Sequence 8179, Ap
1269	61.5	4.4	4.4	470	US-11-330-403-13594	Sequence 13594, A	1342	61	4.4	350	6	US-10-449-902-56491	Sequence 56491, A
1270	61.5	4.4	4.4	484	US-11-056-355B-96202	Sequence 96202, A	1343	61	4.4	355	7	US-11-133-140-6	Sequence 6, Appl
1271	61.5	4.4	4.4	490	US-11-330-403-8766	Sequence 8766, Ap	1344	61	4.4	357	6	US-10-449-902-29928	Sequence 29928, A
1272	61.5	4.4	4.4	496	US-10-953-349-2647	Sequence 2647, Ap	1345	61	4.4	357	6	US-11-056-355B-11072	Sequence 11072, A
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1274	61.5	4.4	4.4	498	US-11-330-403-13592	Sequence 13592, A	1347	61	4.4	360	6	US-11-056-355B-64645	Sequence 64645, A
1275	61.5	4.4	4.4	507	US-11-296-657-14	Sequence 14, Appl	1348	61	4.4	362	7	US-11-175-714-134	Sequence 134, App
1276	61.5	4.4	4.4	512	US-11-056-355B-106720	Sequence 106720, A	1349	61	4.4	367	6	US-10-471-571A-3160	Sequence 3160, Ap
1277	61.5	4.4	4.4	512	US-11-056-355B-117959	Sequence 117959, A	1350	61	4.4	373	7	US-11-312-958-10	Sequence 10, Appl
1278	61.5	4.4	4.4	529	US-11-056-355B-106719	Sequence 106719, A	1351	61	4.4	386	7	US-11-056-355B-43989	Sequence 43989, A
1279	61.5	4.4	4.4	529	US-11-056-355B-117958	Sequence 117958, A	1352	61	4.4	389	7	US-11-056-355B-5745	Sequence 5745, Ap
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1281	61.5	4.4	4.4	548	US-11-330-403-11180	Sequence 11180, A	1354	61	4.4	398	7	US-11-056-355B-22682	Sequence 22682, A
1282	61.5	4.4	4.4	581	US-10-449-902-48535	Sequence 48535, A	1355	61	4.4	398	7	US-11-056-355B-43988	Sequence 43988, A
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1284	61.5	4.4	4.4	590	US-11-296-657-52	Sequence 52, Appl	1357	61	4.4	414	7	US-11-056-355B-8178	Sequence 8178, Ap
1285	61.5	4.4	4.4	590	US-11-296-657-53	Sequence 53, Appl	1358	61	4.4	419	7	US-11-056-355B-10757	Sequence 10757, A
1286	61.5	4.4	4.4	597	US-11-330-403-3154	Sequence 3154, Ap	1359	61	4.4	432	7	US-11-056-355B-8177	Sequence 8177, Ap
1287	61.5	4.4	4.4	626	US-10-515-919A-16	Sequence 16, Appl	1360	61	4.4	446	7	US-11-056-355B-43987	Sequence 43987, A
1288	61.5	4.4	4.4	626	US-10-515-919A-21	Sequence 21, Appl	1361	61	4.4	446	7	US-11-056-355B-81526	Sequence 81526, A
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1290	61.5	4.4	4.4	666	US-10-449-902-45247	Sequence 45247, A	1363	61	4.4	450	7	US-11-056-355B-10756	Sequence 10756, A
1291	61.5	4.4	4.4	680	US-10-449-902-34793	Sequence 34793, A	1364	61	4.4	457	7	US-11-330-403-3994	Sequence 3994, Ap
1292	61.5	4.4	4.4	686	US-10-539-228-331	Sequence 331, App	1365	61	4.4	488	6	US-11-330-403-18422	Sequence 18422, A
1293	61.5	4.4	4.4	690	US-11-056-355B-85441	Sequence 85441, A	1366	61	4.4	489	6	US-10-449-902-52773	Sequence 52773, A
1294	61.5	4.4	4.4	696	US-11-056-355B-85440	Sequence 85440, A	1367	61	4.4	496	6	US-11-056-355B-81525	Sequence 81525, A
1295	61.5	4.4	4.4	703	US-10-449-902-35762	Sequence 35762, A	1368	61	4.4	500	6	US-10-449-902-52244	Sequence 52244, A
1296	61.5	4.4	4.4	738	US-10-539-228-571	Sequence 571, App	1369	61	4.4	502	7	US-11-056-355B-81524	Sequence 81524, A
1297	61.5	4.4	4.4	771	US-11-056-355B-85439	Sequence 85439, A	1370	61	4.4	542	7	US-11-316-042-30	Sequence 30, Appl
1298	61.5	4.4	4.4	791	US-10-449-902-45527	Sequence 45527, A	1371	61	4.4	542	7	US-11-121-154-81	Sequence 81, Appl
1299	61.5	4.4	4.4	1011	US-10-449-902-53046	Sequence 53046, A	1372	61	4.4	738	6	US-10-518-941-27	Sequence 27, Appl
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1301	61.5	4.4	4.4	1076	US-10-449-902-35762	Sequence 35762, A	1374	61	4.4	754	6	US-10-471-571A-2544	Sequence 2544, Ap
1302	61.5	4.4	4.4	1086	US-11-325-276-10	Sequence 10, Appl	1375	61	4.4	818	6	US-10-449-902-47207	Sequence 47207, A
1303	61.5	4.4	4.4	1315	US-10-449-902-52692	Sequence 52692, A	1376	61	4.4	818	6	US-10-449-902-53444	Sequence 53444, A
1304	61.5	4.4	4.4	2192	US-11-335-891-27	Sequence 27, Appl	1377	61	4.4	830	6	US-10-449-902-48556	Sequence 48556, A
1305	61	4.4	4.4	2192	US-11-333-747A-116	Sequence 116, App	1378	61	4.4	1065	7	US-11-121-133-239	Sequence 239, App
1306	61	4.4	4.4	211	US-11-056-355B-82429	Sequence 82429, A	1379	61	4.4	1332	6	US-10-449-902-41138	Sequence 41138, A
1307	61	4.4	4.4	223	US-11-056-355B-82428	Sequence 82428, A	1380	61	4.4	1394	6	US-10-953-349-6031	Sequence 6031, Ap
1308	61	4.4	4.4	230	US-10-449-902-30479	Sequence 30479, A	1381	61	4.4	1407	6	US-10-953-349-6030	Sequence 6030, Ap
1309	61	4.4	4.4	230	US-11-056-355B-56900	Sequence 56900, A	1382	61	4.4	1408	6	US-10-953-349-6029	Sequence 6029, Ap
1310	61	4.4	4.4	231	US-11-056-355B-72118	Sequence 72118, Ap	1383	61	4.4	1503	7	US-11-312-958-48	Sequence 48, Appl
1311	61	4.4	4.4	244	US-10-449-902-48089	Sequence 48089, A	1384	60.5	4.3	190	7	US-11-056-355B-12118	Sequence 12118, A
1312	61	4.4	4.4	252	US-11-056-355B-82427	Sequence 82427, A	1385	60.5	4.3	198	7	US-11-056-355B-70881	Sequence 70881, A
1313	61	4.4	4.4	258	US-10-541-993-26	Sequence 26, Appl	1386	60.5	4.3	203	6	US-10-953-349-26292	Sequence 26292, A
1314	61	4.4	4.4	258	US-10-524-827-2	Sequence 2, Appl	1387	60.5	4.3	203	7	US-11-056-355B-63381	Sequence 63381, A
1315	61	4.4	4.4	258	US-10-568-741-30	Sequence 30, Appl	1388	60.5	4.3	220	7	US-11-056-355B-70880	Sequence 70880, A
1316	61	4.4	4.4	264	US-10-449-902-30587	Sequence 30587, A	1389	60.5	4.3	231	6	US-10-953-349-33070	Sequence 33070, A
1317	61	4.4	4.4	264	US-10-449-902-31618	Sequence 31618, A	1390	60.5	4.3	231	7	US-11-056-355B-6862	Sequence 6862, Ap
1318	61	4.4	4.4	274	US-11-056-355B-7217	Sequence 7217, Ap	1391	60.5	4.3	231	7	US-11-056-355B-11242	Sequence 11242, A
1319	61	4.4	4.4	278	US-10-471-571A-3176	Sequence 3176, Ap	1392	60.5	4.3	231	7	US-11-056-355B-12117	Sequence 12117, A
1320	61	4.4	4.4	290	US-10-953-349-25786	Sequence 25786, A	1393	60.5	4.3	247	6	US-10-196-749-228	Sequence 228, App
1321	61	4.4	4.4	290	US-11-056-355B-64647	Sequence 64647, A	1394	60.5	4.3	262	6	US-10-541-993-28	Sequence 28, Appl
1322	61	4.4	4.4	292	US-10-953-349-25423	Sequence 25423, A	1395	60.5	4.3	262	6	US-10-524-827-8	Sequence 8, Appl
1323	61	4.4	4.4	293	US-11-056-355B-7216	Sequence 7216, Ap	1396	60.5	4.3	262	6	US-10-524-827-10	Sequence 10, Appl
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1326	61	4.4	4.4	295	US-11-056-355B-34977	Sequence 34977, A	1399	60.5	4.3	266	6	US-10-449-902-30766	Sequence 30766, A
1327	61	4.4	4.4	295	US-11-056-355B-99388	Sequence 99388, A	1400	60.5	4.3	266	6	US-10-524-827-70	Sequence 70, Appl
1328	61	4.4	4.4	295	US-11-056-355B-110627	Sequence 110627, A	1401	60.5	4.3	268	6	US-10-953-349-26291	Sequence 26291, A
1329	61	4.4	4.4	297	US-11-330-403-10949	Sequence 10949, A	1402	60.5	4.3	268	6	US-11-056-355B-63380	Sequence 63380, A
1330	61	4.4	4.4	306	US-11-056-355B-3452	Sequence 3452, Ap	1403	60.5	4.3	276	6	US-10-953-349-33069	Sequence 33069, A
1331	61	4.4	4.4	312	US-10-953-349-25422	Sequence 25422, A	1404	60.5	4.3	276	7	US-11-056-355B-6861	Sequence 6861, Ap
1332	61	4.4	4.4	312	US-11-056-355B-5747	Sequence 5747, Ap	1405	60.5	4.3	276	7	US-11-056-355B-11241	Sequence 11241, A
1333	61	4.4	4.4	317	US-10-953-349-25785	Sequence 25785, A	1406	60.5	4.3	276	7	US-11-056-355B-12116	Sequence 12116, A
1334	61	4.4	4.4	317	US-11-056-355B-3451	Sequence 3451, Ap	1407	60.5	4.3	281	7	US-11-056-355B-104252	Sequence 104252, A
1335	61	4.4	4.4	317	US-11-056-355B-64646	Sequence 64646, A	1408	60.5	4.3	281	7	US-11-056-355B-115491	Sequence 115491, A
1336	61	4.4	4.4	326	US-11-106-014-96	Sequence 96, Appl	1409	60.5	4.3	283	6	US-10-471-571A-5166	Sequence 5166, Ap
1337	61	4.4	4.4	326	US-11-056-355B-5746	Sequence 5746, Ap	1410	60.5	4.3	284	6	US-10-449-902-38334	Sequence 38334, A
1338	61	4.4	4.4	327	US-11-330-403-4527	Sequence 4527, Ap	1411	60.5	4.3	286	7	US-11-056-355B-76624	Sequence 76624, A
1339	61	4.4	4.4	335	US-11-056-355B-3450	Sequence 3450, Ap	1412	60.5	4.3	289	6	US-10-449-902-32570	Sequence 32570, A

1413	60.5	4.3	294	6	US-10-449-902-45611	Sequence 45611, A	1486	60.5	4.3	460	7	US-11-056-355B-48860	Sequence 48860, A
1414	60.5	4.3	295	7	US-11-056-355B-12647	Sequence 12647, A	1487	60.5	4.3	460	7	US-11-056-355B-97951	Sequence 97951, A
1415	60.5	4.3	296	7	US-11-056-355B-11240	Sequence 11240, A	1488	60.5	4.3	460	7	US-11-056-355B-109190	Sequence 109190, A
1416	60.5	4.3	300	6	US-10-953-349-33068	Sequence 33068, A	1489	60.5	4.3	466	7	US-11-056-355B-88021	Sequence 88021, A
1417	60.5	4.3	300	7	US-11-056-355B-6860	Sequence 6860, Ap	1490	60.5	4.3	467	7	US-11-056-355B-65332	Sequence 65332, A
1418	60.5	4.3	304	7	US-11-056-355B-22249	Sequence 22249, A	1491	60.5	4.3	469	7	US-11-330-403-4890	Sequence 4890, Ap
1419	60.5	4.3	305	6	US-10-953-349-23037	Sequence 23037, A	1492	60.5	4.3	469	7	US-11-330-403-12483	Sequence 12483, A
1420	60.5	4.3	318	7	US-11-056-355B-103355	Sequence 103355, A	1493	60.5	4.3	470	7	US-11-056-355B-75678	Sequence 75678, A
1421	60.5	4.3	318	7	US-11-056-355B-114594	Sequence 114594, A	1494	60.5	4.3	471	7	US-11-056-355B-90040	Sequence 90040, A
1422	60.5	4.3	318	6	US-10-449-902-31611	Sequence 31611, A	1495	60.5	4.3	471	7	US-11-056-355B-93796	Sequence 93796, A
1423	60.5	4.3	326	6	US-10-449-902-32247	Sequence 32247, A	1496	60.5	4.3	472	6	US-10-471-571A-4034	Sequence 4034, Ap
1424	60.5	4.3	326	6	US-10-449-902-42853	Sequence 42853, A	1497	60.5	4.3	480	7	US-11-330-403-6640	Sequence 6640, Ap
1425	60.5	4.3	328	7	US-11-056-355B-103354	Sequence 103354, A	1498	60.5	4.3	482	6	US-10-449-903-35736	Sequence 35736, A
1426	60.5	4.3	328	7	US-11-056-355B-114593	Sequence 114593, A	1499	60.5	4.3	483	7	US-11-056-355B-90039	Sequence 90039, A
1427	60.5	4.3	331	6	US-10-471-571A-1932	Sequence 1932, Ap	1500	60.5	4.3	483	7	US-11-056-355B-93795	Sequence 93795, A
1428	60.5	4.3	331	7	US-11-024-545-2	Sequence 2, Appl							
1429	60.5	4.3	331	7	US-11-190-750-30	Sequence 30, Appl							
1430	60.5	4.3	331	7	US-11-264-784-96	Sequence 96, Appl							
1431	60.5	4.3	331	7	US-11-264-737-137	Sequence 137, App							
1432	60.5	4.3	331	7	US-11-265-761-109	Sequence 109, App							
1433	60.5	4.3	336	6	US-10-953-349-26290	Sequence 26290, A							
1434	60.5	4.3	336	7	US-11-056-355B-63379	Sequence 63379, A							
1435	60.5	4.3	339	7	US-11-056-355B-12646	Sequence 12646, A							
1436	60.5	4.3	341	6	US-10-449-902-44479	Sequence 44479, A							
1437	60.5	4.3	341	7	US-11-056-355B-39245	Sequence 39245, A							
1438	60.5	4.3	348	7	US-11-056-355B-103353	Sequence 103353, A							
1439	60.5	4.3	348	7	US-11-056-355B-114592	Sequence 114592, A							
1440	60.5	4.3	349	7	US-11-330-403-2421	Sequence 2421, Ap							
1441	60.5	4.3	355	7	US-11-056-355B-12645	Sequence 12645, A							
1442	60.5	4.3	357	7	US-11-330-403-2989	Sequence 2989, Ap							
1443	60.5	4.3	358	7	US-11-056-355B-39244	Sequence 39244, A							
1444	60.5	4.3	358	7	US-11-056-355B-39243	Sequence 39243, A							
1445	60.5	4.3	375	7	US-11-358-841-3	Sequence 3, Appl							
1446	60.5	4.3	375	7	US-11-333-830-17	Sequence 17, Appl							
1447	60.5	4.3	380	6	US-10-471-571A-3466	Sequence 3466, Ap							
1448	60.5	4.3	388	6	US-11-056-355B-65333	Sequence 65333, A							
1449	60.5	4.3	391	6	US-10-449-902-33014	Sequence 33014, A							
1450	60.5	4.3	393	6	US-10-953-349-10167	Sequence 10167, A							
1451	60.5	4.3	393	7	US-11-056-355B-47454	Sequence 47454, A							
1452	60.5	4.3	393	7	US-11-056-355B-98411	Sequence 98411, A							
1453	60.5	4.3	393	7	US-11-056-355B-109650	Sequence 109650, A							
1454	60.5	4.3	406	6	US-10-953-349-21790	Sequence 21790, A							
1455	60.5	4.3	406	7	US-11-056-355B-57273	Sequence 57273, A							
1456	60.5	4.3	406	7	US-11-330-403-6274	Sequence 6274, Ap							
1457	60.5	4.3	406	7	US-11-330-403-12480	Sequence 12480, A							
1458	60.5	4.3	408	7	US-11-226-554-146	Sequence 146, App							
1459	60.5	4.3	408	7	US-11-248-718-146	Sequence 146, App							
1460	60.5	4.3	421	7	US-11-330-403-14758	Sequence 14758, A							
1461	60.5	4.3	423	6	US-10-953-349-14523	Sequence 14523, A							
1462	60.5	4.3	423	7	US-11-174-307B-3500	Sequence 3500, Ap							
1463	60.5	4.3	423	7	US-11-056-355B-59935	Sequence 59935, A							
1464	60.5	4.3	424	6	US-10-953-349-11588	Sequence 11588, A							
1465	60.5	4.3	424	7	US-11-056-355B-48861	Sequence 48861, A							
1466	60.5	4.3	424	7	US-11-056-355B-97952	Sequence 97952, A							
1467	60.5	4.3	424	7	US-11-056-355B-109191	Sequence 109191, A							
1468	60.5	4.3	429	6	US-10-953-349-14522	Sequence 14522, A							
1469	60.5	4.3	429	7	US-11-056-355B-59934	Sequence 59934, A							
1470	60.5	4.3	430	6	US-10-953-349-6077	Sequence 6077, Ap							
1471	60.5	4.3	430	7	US-11-056-355B-23540	Sequence 23540, A							
1472	60.5	4.3	430	7	US-11-056-355B-33130	Sequence 33130, A							
1473	60.5	4.3	430	7	US-11-056-355B-88022	Sequence 88022, A							
1474	60.5	4.3	437	7	US-11-056-355B-38167	Sequence 38167, A							
1475	60.5	4.3	437	7	US-11-056-355B-76967	Sequence 76967, A							
1476	60.5	4.3	448	7	US-11-330-403-8723	Sequence 8723, Ap							
1477	60.5	4.3	448	7	US-11-056-355B-97273	Sequence 97273, A							
1478	60.5	4.3	452	6	US-10-471-571A-3560	Sequence 3560, Ap							
1479	60.5	4.3	453	7	US-11-056-355B-75679	Sequence 75679, A							
1480	60.5	4.3	453	7	US-11-330-403-17108	Sequence 17108, A							
1481	60.5	4.3	453	7	US-11-330-403-17179	Sequence 17179, A							
1482	60.5	4.3	454	6	US-10-449-902-49028	Sequence 49028, A							
1483	60.5	4.3	456	7	US-11-330-403-10986	Sequence 10986, A							
1484	60.5	4.3	457	7	US-11-330-403-12703	Sequence 12703, A							
1485	60.5	4.3	460	6	US-10-953-349-11587	Sequence 11587, A							

ALIGNMENTS

RESULT 1

US-10-196-749-10

; Sequence 10, Application US/10196749

; Publication No. US20060094864A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Chen, Jian

; APPLICANT: Desnoyers, Luc

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Pan, James

; APPLICANT: Smith, Victoria

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; FILE REFERENCE: P34301C340

; CURRENT FILING DATE: 2002-07-16

; PRIOR APPLICATION NUMBER: US/10/196,749

; PRIOR FILING DATE: 2002-01-15

; PRIOR APPLICATION NUMBER: 60/059263

; PRIOR FILING DATE: 1997-09-18

; PRIOR APPLICATION NUMBER: 60/059266

; PRIOR FILING DATE: 1997-09-18

; PRIOR APPLICATION NUMBER: 60/062250

; PRIOR FILING DATE: 1997-10-17

; PRIOR APPLICATION NUMBER: 60/063120

; PRIOR FILING DATE: 1997-10-24

; PRIOR APPLICATION NUMBER: 60/063121

; PRIOR FILING DATE: 1997-10-24

; PRIOR APPLICATION NUMBER: 60/063486

; PRIOR FILING DATE: 1997-10-21

; PRIOR APPLICATION NUMBER: 60/063540

; PRIOR FILING DATE: 1997-10-28

; PRIOR APPLICATION NUMBER: 60/063541

; PRIOR FILING DATE: 1997-10-28

; PRIOR APPLICATION NUMBER: 60/063544

; PRIOR FILING DATE: 1997-10-28

; NUMBER OF SEQ ID NOS: 612

; SEQ ID NO 10

; LENGTH: 266

; TYPE: PRT

; ORGANISM: Homo Sapien

US-10-196-749-10

Query Match 100.0%; Score 1392; DB 6; Length 266;

Best Local Similarity 100.0%; Pred. No. 4.9e-117; Indels 0; Gaps 0;

Matches 266; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMWFOGSLFPLSALVWTSAAFIYSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAML 60
DB 1 MMWFOGSLFPLSALVWTSAAFIYSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAML 60
QY 61 NIAAVALCIATYVRYKQVHALSPEENVIIKLNKAGLVGLSCLGSLIVANFQKTLFAA 120
DB 61 NIAAVALCIATYVRYKQVHALSPEENVIIKLNKAGLVGLSCLGSLIVANFQKTLFAA 120
QY 121 HVSGAVLTFGMSGLYMFVQTILSYQMPKIHGQVFWIRLLLVWCGVSALSMLTCSVYL 180
DB 121 HVSGAVLTFGMSGLYMFVQTILSYQMPKIHGQVFWIRLLLVWCGVSALSMLTCSVYL 180
QY 181 HSGNFGTDLQKLNWPNEDKGYVLHMITTAAEWSMSFSFGFFLTYYIRDFOKISLRVEAN 240
DB 181 HSGNFGTDLQKLNWPNEDKGYVLHMITTAAEWSMSFSFGFFLTYYIRDFOKISLRVEAN 240
QY 241 LHGLTLYDTAPCPINNERTLLSRDI 266
DB 241 LHGLTLYDTAPCPINNERTLLSRDI 266
RESULT 2
US-11-101-316-2
; Sequence 2, Application US/11101316
; Publication No. US20060099657A1
; GENERAL INFORMATION:
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: ANTIBODIES TO A POLYPEPTIDE ENCODED BY A NUCLEIC ACID
; TITLE OF INVENTION: UNDEREXPRESSED IN MELANOMA
; FILE REFERENCE: P3230R1C17C1
; CURRENT APPLICATION NUMBER: US/11/101,316
; PRIOR FILING DATE: 2005-04-06
; PRIOR APPLICATION NUMBER: 10/063526
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: 10/006867
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: 09/380137
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: 1999-06-02
; PRIOR APPLICATION NUMBER: 60/087759
; PRIOR FILING DATE: 1998-06-02
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 2
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Homo Sapien
US-11-101-316-2
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.9e-117;
Matches 266; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MMWFOGSLFPLSALVWTSAAFIYSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAML 60
DB 1 MMWFOGSLFPLSALVWTSAAFIYSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAML 60
QY 61 NIAAVALCIATYVRYKQVHALSPEENVIIKLNKAGLVGLSCLGSLIVANFQKTLFAA 120
DB 61 NIAAVALCIATYVRYKQVHALSPEENVIIKLNKAGLVGLSCLGSLIVANFQKTLFAA 120
QY 121 HVSGAVLTFGMSGLYMFVQTILSYQMPKIHGQVFWIRLLLVWCGVSALSMLTCSVYL 180
DB 121 HVSGAVLTFGMSGLYMFVQTILSYQMPKIHGQVFWIRLLLVWCGVSALSMLTCSVYL 180
QY 181 HSGNFGTDLQKLNWPNEDKGYVLHMITTAAEWSMSFSFGFFLTYYIRDFOKISLRVEAN 240
DB 181 HSGNFGTDLQKLNWPNEDKGYVLHMITTAAEWSMSFSFGFFLTYYIRDFOKISLRVEAN 240

DB 181 HSGNFGTDLQKLNWPNEDKGYVLHMITTAAEWSMSFSFGFFLTYYIRDFOKISLRVEAN 240
QY 241 LHGLTLYDTAPCPINNERTLLSRDI 266
DB 241 LHGLTLYDTAPCPINNERTLLSRDI 266
RESULT 3
US-11-376-673-2
; Sequence 2, Application US/11376673
; Publication No. US20060160186A1
; GENERAL INFORMATION:
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: A NUCLEIC ACID UNDEREXPRESSED IN STOMACH TUMOR AND
; TITLE OF INVENTION: LUNG TUMOR
; FILE REFERENCE: P3230R1C165C
; CURRENT APPLICATION NUMBER: US/11/376,673
; CURRENT FILING DATE: 2006-03-14
; PRIOR APPLICATION NUMBER: 10/063742
; PRIOR FILING DATE: 2002-05-09
; PRIOR APPLICATION NUMBER: 10/006867
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: 60/170262
; PRIOR FILING DATE: 1999-12-09
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 2
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Homo Sapien
US-11-376-673-2
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.9e-117;
Matches 266; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MMWFOGSLFPLSALVWTSAAFIYSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAML 60
DB 1 MMWFOGSLFPLSALVWTSAAFIYSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAML 60
QY 61 NIAAVALCIATYVRYKQVHALSPEENVIIKLNKAGLVGLSCLGSLIVANFQKTLFAA 120
DB 61 NIAAVALCIATYVRYKQVHALSPEENVIIKLNKAGLVGLSCLGSLIVANFQKTLFAA 120
QY 121 HVSGAVLTFGMSGLYMFVQTILSYQMPKIHGQVFWIRLLLVWCGVSALSMLTCSVYL 180
DB 121 HVSGAVLTFGMSGLYMFVQTILSYQMPKIHGQVFWIRLLLVWCGVSALSMLTCSVYL 180
QY 181 HSGNFGTDLQKLNWPNEDKGYVLHMITTAAEWSMSFSFGFFLTYYIRDFOKISLRVEAN 240
DB 181 HSGNFGTDLQKLNWPNEDKGYVLHMITTAAEWSMSFSFGFFLTYYIRDFOKISLRVEAN 240
QY 241 LHGLTLYDTAPCPINNERTLLSRDI 266
DB 241 LHGLTLYDTAPCPINNERTLLSRDI 266
RESULT 4
US-11-293-697-2867
; Sequence 2867, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260

Query Match 6.7%; Score 93.5; DB 7; Length 303;
Best Local Similarity 21.8%; Pred. No. 0.68; Mismatches 53; Conservative 47; Gaps 9;
Matches 47; Conservative 53; Mismatches 95; Indels 21; Gaps 9;

QY 10 FLPSALVITWTSAAAFISYITAVTLHHIDPALPYISDTGTVAPEKCLFG-AMLNIAA---- 64
DB 14 YIP--LLLLPSSASVESSESSCLKYI--VLIYVLLGVIIAGDNMLYSVGLLYLSASTYS 69
QY 65 VLCIATYVRYKQVHALSPEENVIIKLNKAGVLGILSCGLSIVANFQKTLTFAAHVSG 124
DB 70 LICATQAFNAVFSYFNAQKFTALILNSVLLSFAALIALNDADTPSGVRSKYIVG 129
QY 125 AVLTGMSGLYMFVQITLSYQMPKIHGQVFWIRLLVILVWCGVSALSMLTSCSSVHLHSGN 184
DB 130 FVCTLAASALYSLLLSLMQFSPF-KILKRETFSVLEMQIYTSLVA---TCVSVI--GL 182
QY 185 FGTDLEQKLHWPNE--DKG---YVLHMITTAEWSM 215
DB 183 FASGEWRTLHGEVGHKGQASVYTLVMTAVTQV 218

RESULT 8
US-11-056-355B-83607
; Sequence 83607, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nikolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; FILE REFERENCE: 2750-1590PUS2
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 83607
; LENGTH: 379
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; NAME/KEY: peptide
; LOCATION: (1)..(379)
; OTHER INFORMATION: Ceres Seq. ID no. 12670983
US-11-056-355B-83607

Query Match 6.7%; Score 93.5; DB 7; Length 379;
Best Local Similarity 21.8%; Pred. No. 0.87; Mismatches 53; Conservative 47; Gaps 9;
Matches 47; Conservative 53; Mismatches 95; Indels 21; Gaps 9;

QY 10 FLPSALVITWTSAAAFISYITAVTLHHIDPALPYISDTGTVAPEKCLFG-AMLNIAA---- 64
DB 90 YIP--LLLLPSSASVESSESSCLKYI--VLIYVLLGVIIAGDNMLYSVGLLYLSASTYS 145
QY 65 VLCIATYVRYKQVHALSPEENVIIKLNKAGVLGILSCGLSIVANFQKTLTFAAHVSG 124
DB 146 LICATQAFNAVFSYFNAQKFTALILNSVLLSFAALIALNDADTPSGVRSKYIVG 205
QY 125 AVLTGMSGLYMFVQITLSYQMPKIHGQVFWIRLLVILVWCGVSALSMLTSCSSVHLHSGN 184
DB 206 FVCTLAASALYSLLLSLMQFSPF-KILKRETFSVLEMQIYTSLVA---TCVSVI--GL 258
QY 185 FGTDLEQKLHWPNE--DKG---YVLHMITTAEWSM 215
DB 259 FASGEWRTLHGEVGHKGQASVYTLVMTAVTQV 294

RESULT 9
US-11-056-355B-4953
; Sequence 4953, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:

; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nikolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; FILE REFERENCE: 2750-1590PUS2
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 4953
; LENGTH: 312
; TYPE: prt
; ORGANISM: Zea mays subsp. mays
; NAME/KEY: peptide
; LOCATION: (1)..(312)
; OTHER INFORMATION: Ceres Seq. ID no. 12364515
US-11-056-355B-4953

Query Match 6.3%; Score 88; DB 7; Length 312;
Best Local Similarity 20.4%; Pred. No. 2.2; Mismatches 45; Conservative 61; Indels 102; Gaps 16;
Matches 61; Conservative 45; Mismatches 91; Indels 102; Gaps 16;

QY 4 FQOGLSFLPSALVITWTSAAAFISYITAVTLHHIDPALP--YISDTGTVAPEKCLFGAML- 60
DB 43 FPSAVTYL--ALIPGRITIPFANLITA---GVVEQTIPGMVVSIIIGLL-----LFGKLE 92
QY 61 -----NTAAVLC-----IATYVRYKQVHALSPEENVIIKLNKAGVLGI 100
DB 93 PLWGSKLSKRFIFVNLSTSAVFMATVLYITQEEIYLYTPFSGFY-----GVLSGL 146
QY 101 LSCGLSIVANFQKTLTFAAHV-----SGAVLTFGMSGLYMFVQITLSYQMPKIHGKQ 154
DB 147 L--VGIKQLLPDQELNLFVLKIKAKWIPSLVALISILGSI--FYDFMSY-LPVLIFGY 201
QY 155 VFWRLLLVWCGVSALSMLTSCSSVHLHSGNFGTDLEQKLHWPEDKGYVLHMITTAEWS 214
DB 202 MSWIVLYR-----FQKLETSLKGDPSBE----- 225
QY 215 MSFSPFGFLYIRDFOKISLRV-----EANLHGLTYDTACP-----INNERTR 260
DB 226 --FSFSSFPFVRPFLDPIASVFRHLLCGRSDARGETL-DTSPPLGSDSPFANRRRR 281

RESULT 10
US-11-056-355B-4952
; Sequence 4952, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nikolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; FILE REFERENCE: 2750-1590PUS2
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 4952
; LENGTH: 313
; TYPE: prt
; ORGANISM: Zea mays subsp. mays
; NAME/KEY: peptide
; LOCATION: (1)..(313)
; OTHER INFORMATION: Ceres Seq. ID no. 12364514
US-11-056-355B-4952

Query Match 6.3%; Score 88; DB 7; Length 313;
Best Local Similarity 20.4%; Pred. No. 2.2; Mismatches 45; Conservative 61; Indels 102; Gaps 16;
Matches 61; Conservative 45; Mismatches 91; Indels 102; Gaps 16;

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105	1392	100.0	266	4	US-10-175-740-10	Sequence 10, Appl	178	1392	100.0	266	4	US-10-184-636-10	Sequence 10, Appl
106	1392	100.0	266	4	US-10-175-743-10	Sequence 10, Appl	179	1392	100.0	266	4	US-10-184-640-10	Sequence 10, Appl
107	1392	100.0	266	4	US-10-176-488-10	Sequence 10, Appl	180	1392	100.0	266	4	US-10-184-650-10	Sequence 10, Appl
108	1392	100.0	266	4	US-10-176-492-10	Sequence 10, Appl	181	1392	100.0	266	4	US-10-184-651-10	Sequence 10, Appl
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134	1392	100.0	266	4	US-10-179-510-10	Sequence 10, Appl	207	1392	100.0	266	4	US-10-195-902-10	Sequence 10, Appl
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137	1392	100.0	266	4	US-10-180-546-10	Sequence 10, Appl	210	1392	100.0	266	4	US-10-063-554-2	Sequence 2, Appl
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447	1392	100.0	266	4	US-10-205-894-10	Sequence 10, Appl	Sequence 10, Appl	520	1392	100.0	266	4	US-10-179-526-10	Sequence 10, Appl
448	1392	100.0	266	4	US-10-205-896-10	Sequence 10, Appl	Sequence 10, Appl	521	1392	100.0	266	4	US-10-173-701-10	Sequence 10, Appl
449	1392	100.0	266	4	US-10-205-898-10	Sequence 10, Appl	Sequence 10, Appl	522	1392	100.0	266	4	US-10-179-511-10	Sequence 10, Appl
450	1392	100.0	266	4	US-10-205-901-10	Sequence 10, Appl	Sequence 10, Appl	523	1392	100.0	266	4	US-10-179-518-10	Sequence 10, Appl
451	1392	100.0	266	4	US-10-205-903-10	Sequence 10, Appl	Sequence 10, Appl	524	1392	100.0	266	4	US-10-183-018-10	Sequence 10, Appl
452	1392	100.0	266	4	US-10-206-909-10	Sequence 10, Appl	Sequence 10, Appl	525	1392	100.0	266	4	US-10-184-624-10	Sequence 10, Appl
453	1392	100.0	266	4	US-10-206-910-10	Sequence 10, Appl	Sequence 10, Appl	526	1392	100.0	266	4	US-10-184-657-10	Sequence 10, Appl
454	1392	100.0	266	4	US-10-206-911-10	Sequence 10, Appl	Sequence 10, Appl	527	1392	100.0	266	4	US-10-197-701-10	Sequence 10, Appl
455	1392	100.0	266	4	US-10-206-912-10	Sequence 10, Appl	Sequence 10, Appl	528	1392	100.0	266	4	US-10-197-706-10	Sequence 10, Appl
456	1392	100.0	266	4	US-10-206-913-10	Sequence 10, Appl	Sequence 10, Appl	529	1392	100.0	266	4	US-10-201-857-10	Sequence 10, Appl
457	1392	100.0	266	4	US-10-206-914-10	Sequence 10, Appl	Sequence 10, Appl	530	1392	100.0	266	4	US-10-202-413-10	Sequence 10, Appl
458	1392	100.0	266	4	US-10-206-920-10	Sequence 10, Appl	Sequence 10, Appl	531	1392	100.0	266	4	US-10-202-938-10	Sequence 10, Appl
459	1392	100.0	266	4	US-10-206-921-10	Sequence 10, Appl	Sequence 10, Appl	532	1392	100.0	266	4	US-10-202-940-10	Sequence 10, Appl
460	1392	100.0	266	4	US-10-206-923-10	Sequence 10, Appl	Sequence 10, Appl	533	1392	100.0	266	4	US-10-205-508-10	Sequence 10, Appl
461	1392	100.0	266	4	US-10-206-925-10	Sequence 10, Appl	Sequence 10, Appl	534	1392	100.0	266	4	US-10-205-905-10	Sequence 10, Appl
462	1392	100.0	266	4	US-10-206-926-10	Sequence 10, Appl	Sequence 10, Appl	535	1392	100.0	266	4	US-10-206-918-10	Sequence 10, Appl
463	1392	100.0	266	4	US-10-206-927-10	Sequence 10, Appl	Sequence 10, Appl	536	1392	100.0	266	4	US-10-208-025-10	Sequence 10, Appl
464	1392	100.0	266	4	US-10-207-916-10	Sequence 10, Appl	Sequence 10, Appl	537	1392	100.0	266	4	US-10-063-580-2	Sequence 2, Appl
465	1392	100.0	266	4	US-10-207-917-10	Sequence 10, Appl	Sequence 10, Appl	538	1392	100.0	266	4	US-10-063-557-2	Sequence 2, Appl

685	1392	100.0	266	4	US-10-063-643-2	Sequence 2, Appli	758	1392	100.0	267	3	US-09-305-736-147	Sequence 147, App
686	1392	100.0	266	4	US-10-063-646-2	Sequence 2, Appli	759	1392	100.0	267	3	US-09-818-683-147	Sequence 147, App
687	1392	100.0	266	4	US-10-063-651-2	Sequence 2, Appli	760	1392	100.0	267	3	US-09-818-683-147	Sequence 147, App
688	1392	100.0	266	4	US-10-063-653-2	Sequence 2, Appli	761	1392	100.0	275	4	US-10-276-774-2411	Sequence 2411, Ap
689	1392	100.0	266	4	US-10-063-660-2	Sequence 2, Appli	762	1388	99.7	267	3	US-09-978-360A-702	Sequence 702, App
690	1392	100.0	266	4	US-10-063-665-2	Sequence 2, Appli	763	1388	99.7	267	3	US-09-978-360A-702	Sequence 702, App
691	1392	100.0	266	4	US-10-063-584-2	Sequence 2, Appli	764	1388	99.7	267	4	US-10-319-763-190	Sequence 190, App
692	1392	100.0	266	4	US-10-063-536-2	Sequence 2, Appli	765	595.5	42.8	172	4	US-10-319-763-96	Sequence 96, Appl
693	1392	100.0	266	4	US-10-063-562-2	Sequence 2, Appli	766	486.5	34.9	238	4	US-10-108-260A-2867	Sequence 2867, Ap
694	1392	100.0	266	4	US-10-063-638-2	Sequence 2, Appli	767	480.5	34.5	231	4	US-10-415-188-11	Sequence 11, Appl
695	1392	100.0	266	4	US-10-063-666-2	Sequence 2, Appli	768	461.5	33.2	246	4	US-10-243-552-375	Sequence 975, App
696	1392	100.0	266	4	US-10-063-672-2	Sequence 2, Appli	769	361.5	26.0	246	6	US-11-097-143-7860	Sequence 7860, Ap
697	1392	100.0	266	4	US-10-063-682-2	Sequence 2, Appli	770	358	25.7	69	3	US-09-978-160A-736	Sequence 736, App
698	1392	100.0	266	4	US-10-063-721-2	Sequence 2, Appli	771	358	25.7	69	3	US-09-978-360A-736	Sequence 736, App
699	1392	100.0	266	4	US-10-063-723-2	Sequence 2, Appli	772	358	25.7	69	4	US-10-319-763-130	Sequence 130, App
700	1392	100.0	266	4	US-10-063-514-2	Sequence 2, Appli	773	358	25.7	69	4	US-10-319-763-224	Sequence 224, App
701	1392	100.0	266	4	US-10-063-516-2	Sequence 2, Appli	774	356.5	25.6	200	5	US-10-450-763-58481	Sequence 58481, A
702	1392	100.0	266	4	US-10-063-529-2	Sequence 2, Appli	775	317.5	22.8	180	4	US-10-264-237-2144	Sequence 2144, Ap
703	1392	100.0	266	4	US-10-063-684-2	Sequence 2, Appli	776	251	18.0	132	4	US-10-755-889-453	Sequence 453, App
704	1392	100.0	266	4	US-10-063-688-2	Sequence 2, Appli	777	251	18.0	132	5	US-10-643-795A-100	Sequence 100, App
705	1392	100.0	266	4	US-10-063-520-2	Sequence 2, Appli	778	251	18.0	132	5	US-10-948-518-100	Sequence 100, App
706	1392	100.0	266	4	US-10-063-647-2	Sequence 2, Appli	779	251	18.0	132	5	US-10-631-467-724	Sequence 724, App
707	1392	100.0	266	4	US-10-063-548-2	Sequence 2, Appli	780	214.5	15.4	283	4	US-10-243-552-521	Sequence 521, App
708	1392	100.0	266	4	US-10-063-578-2	Sequence 2, Appli	781	212	15.2	308	5	US-10-712-892A-37	Sequence 37, Appl
709	1392	100.0	266	4	US-10-063-648-2	Sequence 2, Appli	782	180	12.9	308	5	US-10-450-763-47572	Sequence 47572, A
710	1392	100.0	266	4	US-10-063-677-2	Sequence 2, Appli	783	176.5	12.7	466	5	US-10-450-763-46819	Sequence 46819, A
711	1392	100.0	266	4	US-10-063-718-2	Sequence 2, Appli	784	152	10.9	304	4	US-10-131-487A-83	Sequence 83, Appl
712	1392	100.0	266	4	US-10-063-741-2	Sequence 2, Appli	785	151.5	10.9	437	3	US-09-374-046A-66	Sequence 66, Appl
713	1392	100.0	266	4	US-10-063-617-2	Sequence 2, Appli	786	151.5	10.9	437	4	US-10-616-283-66	Sequence 66, Appl
714	1392	100.0	266	4	US-10-063-664-2	Sequence 2, Appli	787	126	9.1	63	4	US-10-243-552-618	Sequence 618, App
715	1392	100.0	266	4	US-10-063-561-2	Sequence 2, Appli	788	118	8.5	21	3	US-09-903-190-20	Sequence 20, Appl
716	1392	100.0	266	4	US-10-063-618-2	Sequence 2, Appli	789	118	8.5	21	4	US-10-319-763-20	Sequence 20, Appl
717	1392	100.0	266	4	US-10-063-657-2	Sequence 2, Appli	790	118	8.5	21	5	US-10-926-683-2	Sequence 20, Appl
718	1392	100.0	266	4	US-10-063-668-2	Sequence 2, Appli	791	118	8.5	21	5	US-10-930-331-20	Sequence 20, Appl
719	1392	100.0	266	4	US-10-195-887-10	Sequence 10, Appl	792	109.5	7.9	369	4	US-10-437-963-163842	Sequence 163842,
720	1392	100.0	266	4	US-10-195-893-10	Sequence 10, Appl	793	106.5	7.7	275	6	US-11-097-143-7491	Sequence 7491, Ap
721	1392	100.0	266	4	US-10-179-509-10	Sequence 10, Appl	794	105	7.5	218	4	US-10-050-704-322	Sequence 322, App
722	1392	100.0	266	4	US-10-194-486-10	Sequence 10, Appl	795	105	7.5	220	4	US-10-798-512-322	Sequence 322, App
723	1392	100.0	266	4	US-10-195-900-10	Sequence 10, Appl	796	105	7.5	218	4	US-10-050-704-309	Sequence 309, App
724	1392	100.0	266	4	US-10-198-759-10	Sequence 10, Appl	797	105	7.5	220	4	US-10-798-512-309	Sequence 309, App
725	1392	100.0	266	4	US-10-205-506-10	Sequence 10, Appl	798	99	7.1	187	4	US-10-050-704-323	Sequence 323, App
726	1392	100.0	266	4	US-10-174-570-10	Sequence 10, Appl	799	99	7.1	187	4	US-10-108-260A-4787	Sequence 4787, Ap
727	1392	100.0	266	4	US-10-183-005-10	Sequence 10, Appl	800	99	7.1	187	4	US-10-798-512-323	Sequence 323, App
728	1392	100.0	266	4	US-10-179-523-10	Sequence 10, Appl	801	98.5	7.1	298	6	US-11-087-099-1769	Sequence 1769, Ap
729	1392	100.0	266	4	US-10-199-463-10	Sequence 10, Appl	802	98.5	7.1	1066	4	US-10-282-122A-73271	Sequence 73271, A
730	1392	100.0	266	4	US-10-202-471-10	Sequence 10, Appl	803	98.5	7.1	1120	4	US-10-282-122A-74904	Sequence 74904, A
731	1392	100.0	266	4	US-10-207-915-10	Sequence 10, Appl	804	98.5	7.1	1120	4	US-10-282-122A-75487	Sequence 75487, A
732	1392	100.0	266	4	US-10-219-538-23	Sequence 23, Appl	805	95.5	6.9	486	6	US-11-087-099-4550	Sequence 4550, Ap
733	1392	100.0	266	4	US-10-264-237-2714	Sequence 2714, Ap	806	95.5	6.9	486	6	US-11-188-298-4204	Sequence 4204, Ap
734	1392	100.0	266	4	US-10-197-709-10	Sequence 10, Appl	807	94.5	6.8	548	4	US-10-282-122A-62037	Sequence 62037, A
735	1392	100.0	266	4	US-10-206-915-10	Sequence 10, Appl	808	94	6.8	269	4	US-10-282-122A-67735	Sequence 67735, A
736	1392	100.0	266	4	US-10-199-670-10	Sequence 10, Appl	809	93	6.7	1120	4	US-10-282-122A-43015	Sequence 43015, A
737	1392	100.0	266	4	US-10-401-401-147	Sequence 147, App	810	92.5	6.6	473	4	US-10-282-122A-75540	Sequence 75540, A
738	1392	100.0	266	4	US-10-201-858-10	Sequence 10, Appl	811	91.5	6.6	118	4	US-10-264-237-1853	Sequence 1853, Ap
739	1392	100.0	266	4	US-10-205-890-10	Sequence 10, Appl	812	91.5	6.6	373	4	US-10-369-493-6097	Sequence 6097, Ap
740	1392	100.0	266	4	US-10-208-024-10	Sequence 10, Appl	813	91.5	6.6	387	5	US-10-650-467-14	Sequence 14, Appl
741	1392	100.0	266	4	US-10-201-853-10	Sequence 10, Appl	814	91	6.5	430	6	US-11-188-298-7677	Sequence 7677, Ap
742	1392	100.0	266	4	US-10-063-745-2	Sequence 2, Appli	815	91	6.5	432	6	US-11-188-298-13929	Sequence 13929, A
743	1392	100.0	266	4	US-10-206-916-10	Sequence 10, Appl	816	91	6.5	438	4	US-10-425-115-29771	Sequence 29771, A
744	1392	100.0	266	5	US-10-972-317-2	Sequence 2, Appli	817	91	6.5	470	6	US-11-188-298-12101	Sequence 12101, A
745	1392	100.0	266	5	US-10-183-001-10	Sequence 10, Appl	818	91	6.5	475	4	US-10-425-115-297768	Sequence 297768,
746	1392	100.0	266	5	US-10-950-374-23	Sequence 23, Appl	819	91	6.5	486	4	US-10-425-114-39247	Sequence 39247, A
747	1392	100.0	266	5	US-10-175-749-10	Sequence 10, Appl	820	91	6.5	486	4	US-10-425-114-50309	Sequence 50309, A
748	1392	100.0	266	5	US-10-180-554-10	Sequence 10, Appl	821	91	6.5	487	4	US-10-425-114-68137	Sequence 68137, A
749	1392	100.0	266	5	US-10-773-236-267	Sequence 267, App	822	90.5	6.5	529	5	US-10-732-923-23864	Sequence 23864, A
750	1392	100.0	266	5	US-10-921-235-56	Sequence 56, Appl	823	90	6.5	283	3	US-09-738-626-3333	Sequence 3533, Ap
751	1392	100.0	266	5	US-10-063-703-2	Sequence 2, Appli	824	90	6.5	283	4	US-10-627-476-588	Sequence 588, App
752	1392	100.0	266	5	US-10-195-883-10	Sequence 10, Appl	825	90	6.5	283	6	US-11-082-389-252	Sequence 252, App
753	1392	100.0	266	5	US-10-195-888-10	Sequence 10, Appl	826	90	6.5	505	5	US-11-082-389-254	Sequence 254, App
754	1392	100.0	266	5	US-10-194-487-10	Sequence 10, Appl	827	90	6.5	505	5	US-10-741-849-7040	Sequence 7040, Ap
755	1392	100.0	266	5	US-10-195-889-10	Sequence 10, Appl	828	90	6.5	554	6	US-11-188-298-17174	Sequence 17174, A
756	1392	100.0	266	6	US-11-102-240-2	Sequence 2, Appli	829	89.5	6.4	458	4	US-10-282-122A-73461	Sequence 73461, A
757	1392	100.0	266	6	US-11-102-195-2	Sequence 2, Appli	830	89	6.4	330	6	US-11-087-099-8090	Sequence 8090, Ap

831	89	6.4	428	4	US-10-282-122A-78330	Sequence 78330, A	904	84.5	6.1	453	3	US-09-990-436-73	Sequence 73, Appl
832	89	6.4	642	4	US-10-282-122A-51332	Sequence 51332, A	905	84.5	6.1	453	3	US-09-993-687-73	Sequence 73, Appl
833	89	6.4	757	4	US-10-168-428-4	Sequence 4, Appl	906	84.5	6.1	453	3	US-09-989-734-73	Sequence 73, Appl
834	89	6.4	1124	4	US-10-311-623-3	Sequence 3, Appl	907	84.5	6.1	453	3	US-09-997-653-73	Sequence 73, Appl
835	89	6.4	1203	4	US-10-094-749-2651	Sequence 2651, Ap	908	84.5	6.1	453	3	US-09-989-724-73	Sequence 73, Appl
836	88.5	6.4	372	4	US-10-425-114-66797	Sequence 66797, A	909	84.5	6.1	453	3	US-09-989-728-73	Sequence 73, Appl
837	88	6.3	312	6	US-11-096-568A-18337	Sequence 18337, A	910	84.5	6.1	453	3	US-09-990-441-73	Sequence 73, Appl
838	88	6.3	313	6	US-11-087-099-7773	Sequence 7773, Ap	911	84.5	6.1	453	3	US-09-993-667-73	Sequence 73, Appl
839	88	6.3	313	6	US-11-096-568A-18336	Sequence 18336, A	912	84.5	6.1	453	3	US-09-997-428-73	Sequence 73, Appl
840	88	6.3	437	6	US-11-087-099-9904	Sequence 9904, Ap	913	84.5	6.1	453	3	US-09-997-666-73	Sequence 73, Appl
841	88	6.3	909	4	US-10-437-963-151932	Sequence 151932, A	914	84.5	6.1	453	3	US-09-990-438-73	Sequence 73, Appl
842	87.5	6.3	233	4	US-10-282-122A-47021	Sequence 47021, A	915	84.5	6.1	453	3	US-09-990-562-73	Sequence 73, Appl
843	87.5	6.3	322	4	US-10-391-363A-1	Sequence 1, Appl	916	84.5	6.1	453	3	US-09-990-711-73	Sequence 73, Appl
844	87.5	6.3	380	6	US-11-087-099-1038	Sequence 1038, Ap	917	84.5	6.1	453	3	US-09-989-726-73	Sequence 73, Appl
845	87.5	6.3	453	3	US-09-972-211-117	Sequence 117, App	918	84.5	6.1	453	3	US-09-998-156-73	Sequence 73, Appl
846	87.5	6.3	453	4	US-10-096-625-117	Sequence 117, App	919	84.5	6.1	453	3	US-09-990-437-73	Sequence 73, Appl
847	87.5	6.3	482	4	US-10-369-923-17652	Sequence 17652, A	920	84.5	6.1	453	3	US-09-991-157-73	Sequence 73, Appl
848	87.5	6.3	482	5	US-10-732-923-11199	Sequence 11199, A	921	84.5	6.1	453	3	US-09-997-514-73	Sequence 73, Appl
849	87.5	6.3	540	5	US-10-732-923-22268	Sequence 22268, A	922	84.5	6.1	453	3	US-09-997-573-73	Sequence 73, Appl
850	87	6.2	273	4	US-10-425-115-223282	Sequence 223282, A	923	84.5	6.1	453	3	US-09-991-172-73	Sequence 73, Appl
851	87	6.2	580	6	US-11-188-298-9465	Sequence 9465, Ap	924	84.5	6.1	453	3	US-09-990-726-73	Sequence 73, Appl
852	86.5	6.2	239	4	US-10-282-122A-61467	Sequence 61467, A	925	84.5	6.1	453	3	US-09-997-559-73	Sequence 73, Appl
853	86.5	6.2	261	5	US-10-795-159-697	Sequence 697, App	926	84.5	6.1	453	3	US-09-997-601-73	Sequence 73, Appl
854	86.5	6.2	400	4	US-10-369-493-23072	Sequence 23072, A	927	84.5	6.1	453	3	US-09-990-443-73	Sequence 73, Appl
855	86.5	6.2	400	5	US-10-732-923-11195	Sequence 11195, A	928	84.5	6.1	453	3	US-09-991-854-73	Sequence 73, Appl
856	86.5	6.2	485	6	US-11-098-686-10507	Sequence 10507, A	929	84.5	6.1	453	3	US-09-997-628-73	Sequence 73, Appl
857	86.5	6.2	593	6	US-11-045-004-422	Sequence 422, App	930	84.5	6.1	453	3	US-09-997-683-73	Sequence 73, Appl
858	86	6.2	396	3	US-09-741-669-395	Sequence 395, App	931	84.5	6.1	453	3	US-09-989-729A-73	Sequence 73, Appl
859	86	6.2	396	4	US-10-282-122A-47222	Sequence 47222, A	932	84.5	6.1	453	3	US-09-997-349-73	Sequence 73, Appl
860	85.5	6.1	295	4	US-10-282-122A-65159	Sequence 65159, A	933	84.5	6.1	453	3	US-09-997-440-73	Sequence 73, Appl
861	85.5	6.1	295	5	US-10-467-657-23354	Sequence 2354, Ap	934	84.5	6.1	453	3	US-09-990-440-73	Sequence 73, Appl
862	85.5	6.1	311	5	US-10-483-512-32	Sequence 32, Appl	935	84.5	6.1	453	3	US-09-997-469-73	Sequence 73, Appl
863	85.5	6.1	545	3	US-09-374-046A-26	Sequence 26, Appl	936	84.5	6.1	453	3	US-09-993-452-73	Sequence 73, Appl
864	85.5	6.1	545	4	US-10-616-263-26	Sequence 26, Appl	937	84.5	6.1	453	3	US-09-997-542-73	Sequence 73, Appl
865	85.5	6.1	579	5	US-10-755-466-4	Sequence 4, Appl	938	84.5	6.1	453	3	US-09-993-748-73	Sequence 73, Appl
866	85.5	6.1	582	5	US-10-755-466-2	Sequence 2, Appl	944	84.5	6.1	453	3	US-09-992-521-73	Sequence 73, Appl
867	85.5	6.1	700	6	US-11-097-143-34104	Sequence 34104, A	949	84.5	6.1	453	3	US-09-990-439-73	Sequence 73, Appl
868	85	6.1	265	6	US-11-006-098-46	Sequence 46, Appl	941	84.5	6.1	453	3	US-09-989-328-73	Sequence 73, Appl
869	85	6.1	338	4	US-10-282-122A-62710	Sequence 62710, A	942	84.5	6.1	453	3	US-09-993-583-73	Sequence 73, Appl
870	85	6.1	384	4	US-10-282-122A-64468	Sequence 64468, A	943	84.5	6.1	453	3	US-09-941-992-73	Sequence 73, Appl
871	85	6.1	384	4	US-10-437-963-167436	Sequence 167436, A	944	84.5	6.1	453	3	US-09-992-521-73	Sequence 73, Appl
872	85	6.1	419	3	US-09-948-774-2	Sequence 2, Appl	945	84.5	6.1	453	3	US-09-997-333-73	Sequence 73, Appl
873	85	6.1	419	6	US-09-738-626-4556	Sequence 4556, Ap	946	84.5	6.1	453	3	US-09-997-384-73	Sequence 73, Appl
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; Patent No. US20020072067A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Iuc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austen L.
; APPLICANT: Kijavich, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC63
; CURRENT APPLICATION NUMBER: US/09/989,722
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
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; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/087106
; PRIOR FILING DATE: 1998-05-28
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; Sequence 23, Application US/09989723
; Patent No. US20020072092A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Pan L.
; APPLICANT: Ferrara, Napoleone
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; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC62
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; CURRENT FILING DATE: 2001-11-19
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; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 1392; DB 3; Length 266;
Best Local Similarity 100.0%; Pred. No. 5.1e-127;
Matches 266; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 61 NIAAVLCIATYVRYKQVHALSPENVIIKLNKAGLVILGILSCLGLSIVANFQKTLTFAA 120
Db 61 NIAAVLCIATYVRYKQVHALSPENVIIKLNKAGLVILGILSCLGLSIVANFQKTLTFAA 120

Qy 121 HVSQAVLTFMGSLYMFVQTILSYQMOPKIHGKQVFWIRLLLVWCGVSALSMLTCSVYL 180
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Db 181 HSGNFGTDLEQKLHWNPDKGVLHMTTAAEWSNSFSFGFELTYIRDFOKISURVEAN 240

Qy 241 LHGLTLYDTAPCPINNERTLLSRDI 266
Db 241 LHGLTLYDTAPCPINNERTLLSRDI 266

RESULT 3
US-09-989-279-23
; Sequence 23, Application US/09989279
; Patent No. US20020072496A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Iuc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730PIC56
; CURRENT APPLICATION NUMBER: US/09/989,279
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250

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Query Match      100.0%; Score 1392; DB 3; Length 266;
Best Local Similarity 100.0%; Pred. No. 5.1e-127;
Matches 266; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
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; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
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; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 1392; DB 3; Length 266;
Best Local Similarity 100.0%; Pred. No. 5.1e-127;
Matches 266; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 NIAAVLCIATIVRYKQVHALSPEENVIIKLNKAGLVGLSCLGLSIVANFQKTLFAA 120

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Db 121 HVSGAVLTFGMSLYMFVQTILSYQMPKIHGKQVFWIRLLLVICGVSALSMLTSSVL 180

Qy 181 HSGNFGTLEOKLHNWPKDGVVLMHMTTAAEWSMFSFSGFFFLTYIRDFQKISURVEAN 240
Db 181 HSGNFGTLEOKLHNWPKDGVVLMHMTTAAEWSMFSFSGFFFLTYIRDFQKISURVEAN 240

Qy 241 LHGLTYDTAPCPINNERTLLSRDI 266
Db 241 LHGLTYDTAPCPINNERTLLSRDI 266

RESULT 5
US-09-989-731-23
; Sequence 23, Application US/09989731
; Patent No. US20020103125A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.

APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
Acids Encoding the Same
FILE REFERENCE: P2730P1C70
CURRENT APPLICATION NUMBER: US/09/989,731
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
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PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090542

APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC57
CURRENT APPLICATION NUMBER: US/09/989,732
CURRENT FILING DATE: 2001-11-19
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PRIOR FILING DATE: 1997-06-16
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PRIOR APPLICATION NUMBER: 60/088202
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088212

Query Match 100.0%; Score 1392; DB 3; Length 266;
Best Local Similarity 100.0%; Pred. No. 5, 1e-127;
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DB 1 MMWFOGSLFSPALVINTSAAFISYITAVTLHHIDPALPYISDTGTVAPEKCLFGAML 60
QY 61 NTAAVLCIATIIYRYKQVHALSPEENVIIKLNKAGLVGLILSCGLSLSIYANFQKTLFAA 120
DB 61 NTAAVLCIATIIYRYKQVHALSPEENVIIKLNKAGLVGLILSCGLSLSIYANFQKTLFAA 120
QY 121 HVS GAVLTGMSGLYMFVOTILSYQMPKIHGQVFWIRLLLVICGVSALSMLTCSVYL 180
DB 121 HVS GAVLTGMSGLYMFVOTILSYQMPKIHGQVFWIRLLLVICGVSALSMLTCSVYL 180
QY 181 HSGNFGTDLQKHLWNPDKGYVLLHMTTAAEWSMSFSFFGFLTYIRDFOKISLRVEAN 240
DB 181 HSGNFGTDLQKHLWNPDKGYVLLHMTTAAEWSMSFSFFGFLTYIRDFOKISLRVEAN 240
QY 241 LHGLTYDTPACPINNERTLLSRDI 266
DB 241 LHGLTYDTPACPINNERTLLSRDI 266

RESULT 6
US-09-989-732-23
Sequence 23, Application US/099899732
Patent No. US20020123463A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnovers, Luc
APPLICANT: Eaton, Dan L.

; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088217
; PRIOR FILING DATE: 1998-06-05
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; PRIOR FILING DATE: 1998-06-09
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 1392; DB 3; Length 266;
Best Local Similarity 100.0%; Pred. No. 5.1e-127;
Matches 266; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 241 LHGLTYDTAPCPINNERTLLSRDI 266

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; Sequence 23, Application US/09991073
; Patent No. US20020127576A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
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; APPLICANT: Godowski, Paul J.
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; APPLICANT: Gurney, Austin L.
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; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
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; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC15
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; CURRENT FILING DATE: 2001-11-14
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;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 1392; DB 3; Length 266;
Best Local Similarity 100.0%; Pred. No. 5.1e-127;
Matches 266; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MWVFOGSLPLSALVITWTSAAIFSVITAVTLHHIDPALPYISDTGTVAPEKCLFGAML 60

QY 61 NIAAVLCIATYYRYKQVHALSPEENVIIKLNKAGLVGLTSLCGLSIVANFQKTLFAA 120
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QY 181 HSGNFGTDLBQKLHWPEDKGYVLHMITTAAEWSMSFSFFGFFLTYYRDFQKISLRVEAN 240

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QY 241 LHGLTLYDTAPCPINNERTLLSRDI 266
DB 241 LHGLTLYDTAPCPINNERTLLSRDI 266

RESULT 8
US-09-990-442-23
; Sequence 23, Application US/09990442
; Patent No. US20020132252A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deenoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
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; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C8
; CURRENT APPLICATION NUMBER: US/09/990,442
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; Sequence 23, Application US/09993604
; Patent No. US20020137075A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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; CURRENT FILING DATE: 2001-11-14
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; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
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Query Match 100.0%; Score 1392; DB 3; Length 266;
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Matches 266; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 121 HVSQAVLTFMGSLYMFVQTILSYQMOPKIHGKQVFWIRLLLVICWGSALSMLTCSVYL 180
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QY 181 HSGNFGTDLQKLNHPEDKGYVHLMTTAAEWSMSFSFFGFFLTYYIRDFOKISURVEAN 240
Db 181 HSGNFGTDLQKLNHPEDKGYVHLMTTAAEWSMSFSFSFFGFFLTYYIRDFOKISURVEAN 240

QY 241 LHGLTYDTAPCPINNERTLLSRDI 266
Db 241 LHGLTYDTAPCPINNERTLLSRDI 266

RESULT 12
US-09-989-721-23
; Sequence 23, Application US/09989721
; Patent No. US20020142961A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin

;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; FILE REFERENCE: P2730PIC55
;; CURRENT APPLICATION NUMBER: US/09/989,721

;; PRIOR APPLICATION NUMBER: 60/088861
;; PRIOR FILING DATE: 1998-06-11
;; PRIOR APPLICATION NUMBER: 60/088876
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;; PRIOR APPLICATION NUMBER: 60/090694

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/	PRIOR APPLICATION NUMBER:	60/091982
/	PRIOR FILING DATE:	1998-07-07
/	PRIOR APPLICATION NUMBER:	60/092182
/	PRIOR FILING DATE:	1998-07-09

Query Match	100.0%;	Score
Best Local Similarity	100.0%;	Preferential
Matches 266;	Conservative	0; M

Qy	1	MWFOQGSLFPLPSALVLTWTSAAFI	
Db	1	MWFOQGSLFPLPSALVLTWTSAAFI	
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Db	61	NIAAVLCIATTVYRKQVHALSPES	
Qy	121	HVSGAVLTFPGMSLYMFVQTILSY	
Db	121	HVSGAVLTFPGMSLYMFVQTILSY	
Qy	181	HSGNFGTDLEQLHWNPEDKGYLV	
Db	181	HSGNFGTDLEQLHWNPEDKGYLV	
Qy	241	LHGLTYDTACPPINNERTLLSR	
Db	241	LHGLTYDTACPPINNERTLLSR	

RESULT 13

US-09-992-598-23

/	Sequence 23,	Application US/09992598
/	Patent No.	US20020160384A1
/	GENERAL INFORMATION:	
/	APPLICANT:	Ashkenazi, Avi J.
/	APPLICANT:	Baker, Kevin P.
/	APPLICANT:	Botstein, David
/	APPLICANT:	Deshnoyers, Luc
/	APPLICANT:	Eaton, Dan L.
/	APPLICANT:	Ferrara, Napoleone
/	APPLICANT:	Fong, Sherman
/	APPLICANT:	Gerber, Hanspeter
/	APPLICANT:	Gordtsein, Mary E.
/	APPLICANT:	Goddard, Audrey
/	APPLICANT:	Godowski, Paul J.
/	APPLICANT:	Grimaldi, J. Christopher
/	APPLICANT:	Kljasin, Ivar J.
/	APPLICANT:	Napier, Mary A.

APPLICANT:	Pan,James
APPLICANT:	Faoni,Nicholas F.
APPLICANT:	Roy, Margaret Ann
APPLICANT:	Stewart, Timothy A.
APPLICANT:	Tumas, Daniel
APPLICANT:	Watanabe, Colin K.
APPLICANT:	Williams, P. Mickey
APPLICANT:	Wood, William I.
APPLICANT:	Zhang, Zemin
TITLE OF INVENTION:	Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION:	Acids Encoding the Same
FILE REFERENCE:	P2730P1C20
CURRENT APPLICATION NUMBER:	US/09/992,598
CURRENT FILING DATE:	2001-11-14
PRIOR APPLICATION NUMBER:	60/049787
PRIOR FILING DATE:	1997-06-16
PRIOR APPLICATION NUMBER:	60/062250
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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09
;
Query Match 100.0%; Score 1392; DB 3; Length 266;
Best Local Similarity 100.0%; Pred. No. 5.1e-127;
Matches 266; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MWFOGSLFSLPSALVIWTSAAFIYSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAML 60

Qy 61 NIAAVLCIATIVRYKQVHALSPENVIILKNAKAGLVGLSCLGLSIVANFQKTLFPA 120
Db 61 NIAAVLCIATIVRYKQVHALSPENVIILKNAKAGLVGLSCLGLSIVANFQKTLFPA 120

Qy 121 HVSGAVLTFMGSLYMFVQTILSYQMPKIHGKQVFWIRLLLVIVCGVSALSMLTCS 180
Db 121 HVSGAVLTFMGSLYMFVQTILSYQMPKIHGKQVFWIRLLLVIVCGVSALSMLTCS 180

Qy 181 HSGNFGTDLQKLNHPDKGVVLMITTAASWSMSFSFGFFLTYYIRDFOKISLRVEAN 240
Db 181 HSGNFGTDLQKLNHPDKGVVLMITTAASWSMSFSFGFFLTYYIRDFOKISLRVEAN 240

Qy 241 LHGLTLYDTAPCPINNERTLLSRDI 266
Db 241 LHGLTLYDTAPCPINNERTLLSRDI 266

RESULT 14
US-09-989-293A-23
; Sequence 23, Application US/09989293A
; Patent No. US20020177164A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone

APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanpeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Wary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tuma, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC66
CURRENT APPLICATION NUMBER: US/09/989,293A
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
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PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090445

Sequence 23, Application US/09989735
Publication No. US20020193299A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanapeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
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APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
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APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC61
CURRENT APPLICATION NUMBER: US/09/989,735
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
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PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
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PRIOR FILING DATE: 1997-11-13
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PRIOR APPLICATION NUMBER: 60/088033

Query Match 100.0%; Score 1392; DB 3; Length 266;
Best Local Similarity 100.0%; Pred. No. 5.1e-127;
Matches 266; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MWWFQGLSFLPSALVINTWSAIFSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAML 60
Db 1 MWWFQGLSFLPSALVINTWSAIFSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAML 60
QY 61 NTAAVLCIATIVYRYQVHALSPENVIILKNKAGLVGLISCLGLSIVANFQKTLFPA 120
Db 61 NTAAVLCIATIVYRYQVHALSPENVIILKNKAGLVGLISCLGLSIVANFQKTLFPA 120
QY 121 HVSGLVLTGMSGLSNFYVQTILSYQMKPHGKQVFWIRLLVWCGVSALSLTCSVLT 180
Db 121 HVSGLVLTGMSGLSNFYVQTILSYQMKPHGKQVFWIRLLVWCGVSALSLTCSVLT 180
QY 181 HSGNFGTDLLEQKLHWPEDKGYVLLHMITTAAEWSMSFSFPGFLTIVIRDFQKISLRVEAN 240
Db 181 HSGNFGTDLLEQKLHWPEDKGYVLLHMITTAAEWSMSFSFPGFLTIVIRDFQKISLRVEAN 240
QY 241 LHGLTLYDTAPCPINNERTLLSRDI 266
Db 241 LHGLTLYDTAPCPINNERTLLSRDI 266

RESULT 15
US-09-989-735-23

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; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 1392; DB 3; Length 266;
Best Local Similarity 100.0%; Pred. No. 5.1e-127;
Matches 266; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MWFOGGLSFLPSALVIWTSAAFIYSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAML 60
DB 1 MWFOGGLSFLPSALVIWTSAAFIYSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAML 60
QY 61 NIAAVLCIATIVRYKQVHALSPENVIKLNKAGLVGLISCLGLSIVANFQKTLFAA 120
DB 61 NIAAVLCIATIVRYKQVHALSPENVIKLNKAGLVGLISCLGLSIVANFQKTLFAA 120
QY 121 HVSGAVLTFMGSLYMFVQTILSYQMKIHGKQVFWIRLLIIVICGVSALSMLTCSYVL 180
DB 121 HVSGAVLTFMGSLYMFVQTILSYQMKIHGKQVFWIRLLIIVICGVSALSMLTCSYVL 180
QY 181 HSGNEGTDLQKLNHPEDKGYVTLHMITTAESWSFSFGFFLTIVRDFOKISLRVEAN 240

Db 181 HSCNFGTDLEQKLNWNPEDKGYVLHMITTTAAEWSMSFSFGFELTYIRDFQKISLRVEAN 240
Qy 241 LHGLTLYDTAPCPINNERTLLSRDI 266
Db 241 LHGLTLYDTAPCPINNERTLLSRDI 266

Search completed: August 28, 2006, 17:41:27
Job time : 209 secs

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: August 28, 2006, 17:32:09 ; Search time 41 Seconds
(without alignments)
624.236 Million cell updates/sec

Title: US-10-006-867-2
Perfect score: 1392
Sequence: 1 MWFFQGLSFLPSALVWTS.....YDTAPCINNERTLLSRDI 266

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database :

PIR 80:**

1: PIR1:**

2: PIR2:**

3: PIR3:**

4: PIR4:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	361.5	26.0	246	2	T13747
2	288	20.7	271	2	T13654
3	120	8.6	547	2	C8456
4	103	7.4	332	2	E69312
5	98.5	7.1	1120	2	A10561
6	97	7.0	604	2	E72523
7	96	6.9	495	2	S43882
8	94	6.8	495	1	S16447
9	93.5	6.7	379	2	D96506
10	93.5	6.7	429	2	F71651
11	93	6.7	1120	2	F90693
12	93	6.7	1120	2	B85544
13	93	6.7	1120	2	A64776
14	92.5	6.6	473	2	AE0801
15	91.5	6.6	373	2	T24487
16	91.5	6.6	712	2	T02479
17	90.5	6.5	614	2	E86194
18	90	6.5	400	2	C82503
19	90	6.5	492	2	S59107
20	90	6.5	528	2	S19366
21	89.5	6.4	440	2	B64090
22	89.5	6.4	443	2	AB1706
23	89.5	6.4	495	2	G71019
24	89.5	6.4	599	2	T24333
25	89	6.4	428	2	A10034
26	89	6.4	757	2	T42693
27	88.5	6.4	430	2	E75217
28	88.5	6.4	844	2	T23656
29	88	6.3	1165	2	A46180

30	87.5	6.3	233	2	E70114
31	87.5	6.3	429	2	D82181
32	87.5	6.3	482	2	B69803
33	87.5	6.3	540	2	T24675
34	87	6.2	396	2	B31013
35	87	6.2	396	2	D85857
36	87	6.2	435	2	C95975
37	87	6.2	613	2	C83496
38	86.5	6.2	400	2	C69757
39	86.5	6.2	583	2	AH1151
40	86.5	6.2	770	2	G72589
41	86	6.2	373	2	D89865
42	86	6.2	389	2	G75133
43	86	6.2	396	1	E64987
44	86	6.2	703	2	E86146
45	85.5	6.1	295	2	E81179
46	85.5	6.1	296	2	A80210
47	85.5	6.1	498	2	S78184
48	85	6.1	338	2	G70584
49	85	6.1	443	2	B86849
50	85	6.1	1180	2	A47202
51	84.5	6.1	457	2	T46332
52	84.5	6.1	463	2	A40189
53	84.5	6.1	479	2	D72354
54	84.5	6.1	491	2	T15605
55	84.5	6.1	638	2	T11801
56	84.5	6.1	765	2	T22800
57	84	6.0	318	2	E95218
58	84	6.0	460	2	A1028
59	84	6.0	575	2	B83586
60	84	6.0	597	2	H82328
61	83.5	6.0	261	2	D64166
62	83.5	6.0	295	2	A81927
63	83.5	6.0	521	2	T41621
64	83.5	6.0	638	2	B34285
65	83	6.0	305	2	A81998
66	83	6.0	318	2	C98082
67	83	6.0	427	2	F97790
68	83	6.0	460	2	D75106
69	83	6.0	496	2	B83503
70	83	6.0	637	2	S01509
71	82.5	5.9	391	2	S48967
72	82.5	5.9	418	2	E83175
73	82.5	5.9	452	2	A71877
74	82.5	5.9	494	2	T14246
75	82.5	5.9	596	2	S46001
76	82	5.9	317	2	D84098
77	82	5.9	327	2	A82241
78	82	5.9	356	2	D86408
79	82	5.9	446	2	A38244
80	82	5.9	461	2	H64636
81	82	5.9	548	2	B7423
82	82	5.9	557	2	T41588
83	82	5.9	573	2	T23589
84	82	5.9	693	2	T19598
85	82	5.9	1139	2	A10379
86	81.5	5.9	205	2	D95200
87	81.5	5.9	205	2	C98067
88	81.5	5.9	292	2	A81539
89	81.5	5.9	307	2	H37018
90	81.5	5.9	351	2	C86408
91	81.5	5.9	438	2	B83017
92	81.5	5.9	485	2	T24677
93	81.5	5.9	486	2	S51503
94	81.5	5.9	734	2	T13785
95	81	5.8	293	2	C35892
96	81	5.8	293	2	D71517
97	81	5.8	438	2	H85822
98	81	5.8	479	2	C64878
99	81	5.8	479	2	T44326
100	81	5.8	487	2	E96782
101	81	5.8	544	2	T24633
102	81	5.8	710	2	T12143

hemolysin III (ypl)
GDEF family prote
metabolite transp
hypothetical prote
bicyclomycin resis
bicyclomycin resis
probable polysacch
glutathione-regula
transporter homolo
glycerocephorol
hypothetical prote
hypothetical prote
bicyclomycin resis
F22L4.12 protein -
spermidine/putresc
probable ABC sugar
NADH2 dehydrogenas
phosphate transpor
polysaccharide bios
adenylate cyclase
hypothetical prote
Amino acid permeas
lipopolysaccharide
hypothetical prote
NADH2 dehydrogenas
hypothetical prote
iron-compound ABC
hypothetical prote
probable permease
hypothetical prote
hypothetical prote
probable polyamine
hypothetical prote
NADH2 dehydrogenas
hypothetical prote
putrescine-ornithi
hypothetical prote
probable amino aci
NADH2 dehydrogenas
ethanolaminephosph
probable aromatic
proline/betaine tr
NADH2 dehydrogenas
probable amino aci
hypothetical prote
probable ABC trans
purine permease li
citrate transport
proline/betaine tr
cytochrome-c oxida
probable amino-aci
hypothetical prote
hypothetical prote
probable potassium
conserved hypothet
hypothetical prote
sugar ABC transpor
bacitracin resista
F3H9.12 protein -
probable MFS trans
hypothetical prote
NADH2 dehydrogenas
NADH2 dehydrogenas
probable glycerol-
probable metal tra
probable transport
probable amino aci
hypothetical prote
hypothetical prote
NADH2 dehydrogenas

103	80.5	5.8	359	2	F90055	conserved hypother	176	77.5	5.6	363	2	A72771	hypothetical prote
104	80.5	5.8	385	2	T07130	probable amino aci	177	77.5	5.6	461	2	H85755	probable amino aci
105	80.5	5.8	433	2	AC0043	anaerobic C4-dicar	178	77.5	5.6	464	2	C83605	probable transport
106	80.5	5.8	473	2	G69789	sugar transporter	179	77.5	5.6	479	2	A90863	probable amino aci
107	80.5	5.8	528	2	E81186	L-lactate permease	180	77.5	5.6	499	2	AG0882	probable amino aci
108	80.5	5.8	590	1	ORBYPR	arginine transporter	181	77.5	5.6	506	2	F64862	hypothetical prote
109	80.5	5.8	637	2	T7817R	heme lyase yefJ -	182	77.5	5.6	510	2	D96741	hypothetical prote
110	80.5	5.8	728	2	T13794	NADH2 dehydrogenas	183	77.5	5.6	510	2	E71695	hypothetical prote
111	80	5.7	266	2	G83178	conserved hypother	184	77.5	5.6	513	2	A82432	sodium/solute symp
112	80	5.7	291	2	A97387	hypothetical prote	185	77.5	5.6	526	2	T01853	probable hexose tr
113	80	5.7	291	2	AB2605	hypothetical prote	186	77.5	5.6	532	1	S49345	cytochrome-c oxida
114	80	5.7	429	1	C41903	arsenical pump mem	187	77.5	5.6	535	2	S76103	hypothetical prote
115	80	5.7	702	2	T12141	NADH2 dehydrogenas	188	77.5	5.6	535	2	A69478	NADH2 dehydrogenas
116	80	5.7	902	2	C83964	cation-transportin	189	77.5	5.6	717	2	T46172	phenylalanine ammo
117	80	5.7	1123	2	T48586	hypothetical prote	190	77.5	5.6	1118	2	B83018	conserved hypother
118	79.5	5.7	323	2	T32279	hypothetical prote	191	77	5.5	282	2	AD1231	B. subtilis yxkD p
119	79.5	5.7	405	2	T42992	hypothetical prote	192	77	5.5	332	2	D95973	probable sugar upt
120	79.5	5.7	445	2	S77010	cyclin D - Caenorh	193	77	5.5	417	2	F90270	amino acid permeas
121	79.5	5.7	499	2	F75059	NADH-dehydrogenase	194	77	5.5	438	2	G64962	shikimate transpor
122	79.5	5.7	539	1	S49495	cytochrome-c oxida	195	77	5.5	438	2	B69855	amino acid permeas
123	79.5	5.7	542	2	AG3605	potassium efflux s	196	77	5.5	471	2	H90502	phosphate transpor
124	79.5	5.7	570	2	AH2765	cytochrome-c oxida	197	77	5.5	519	2	U00124	membrane protein S
125	79.5	5.7	598	2	E97546	cytochrome c oxida	198	77	5.5	551	1	A55582	cytochrome-c oxida
126	79.5	5.7	741	2	T13051	NADH2 dehydrogenas	199	77	5.5	579	2	AE2177	hypothetical prote
127	79.5	5.7	831	2	B40204	Na+/H+-exchanging	200	77	5.5	662	2	H84984	bo-type ubiquinol
128	79	5.7	172	2	S55015	NADH2 dehydrogenas	201	77	5.5	710	2	T20635	hypothetical prote
129	79	5.7	183	2	A64009	hypothetical prote	202	77	5.5	739	2	T13038	NADH2 dehydrogenas
130	79	5.7	281	2	T26244	hypothetical prote	203	77	5.5	749	2	E71275	hypothetical integ
131	79	5.7	293	2	B83783	hypothetical prote	204	77	5.5	915	2	H96709	hypothetical prote
132	79	5.7	293	2	H72064	ABC transporter, p	205	77	5.5	936	2	T26521	hypothetical prote
133	79	5.7	293	2	C86558	metal transport pr	206	76.5	5.5	152	2	C72681	hypothetical prote
134	79	5.7	307	2	C81862	conserved hypother	207	76.5	5.5	269	2	H69768	conserved hypother
135	79	5.7	377	2	T49063	nodulin-like prote	208	76.5	5.5	284	2	G64052	probable formate t
136	79	5.7	390	2	H72265	hypothetical prote	209	76.5	5.5	289	2	T02035	transmembrane prot
137	79	5.7	395	2	D69312	molybdopterin oxid	210	76.5	5.5	300	2	S40858	hypothetical 32.9K
138	79	5.7	410	2	E84998	hypothetical prote	211	76.5	5.5	300	2	H91233	probable transport
139	79	5.7	438	2	B90976	shikimate transpor	212	76.5	5.5	300	2	H86080	probable transport
140	79	5.7	444	2	G82392	conserved hypother	213	76.5	5.5	301	2	B82235	conserved hypother
141	79	5.7	453	2	AF1198	conserved hypother	214	76.5	5.5	301	2	T27585	hypothetical prote
142	79	5.7	473	2	T31717	hypothetical prote	215	76.5	5.5	305	2	D83699	hypothetical prote
143	79	5.7	489	2	B97289	lysine-specific pe	216	76.5	5.5	334	2	A75142	oligopeptide trans
144	79	5.7	685	2	T12139	NADH2 dehydrogenas	217	76.5	5.5	370	2	AB3334	daunorubicin resis
145	79	5.7	819	2	G69801	hypothetical prote	218	76.5	5.5	377	2	C89456	hypothetical prote
146	79	5.7	2198	2	T20371	hypothetical prote	219	76.5	5.5	382	2	B82177	protein F55A4.8 li
147	78.5	5.6	169	2	H84191	hypothetical prote	220	76.5	5.5	395	2	AD0678	Na+/H+ antiporter
148	78.5	5.6	241	2	S00836	mcB protein - Esc	221	76.5	5.5	431	2	H84069	probable membrane
149	78.5	5.6	366	2	C64449	cationic amino aci	222	76.5	5.5	435	2	F64119	hypothetical prote
150	78.5	5.6	405	2	T26678	hypothetical prote	223	76.5	5.5	474	2	E89643	NAD(P) transhydrog
151	78.5	5.6	412	2	G89773	hypothetical prote	224	76.5	5.5	475	2	AD0402	histidine permease
152	78.5	5.6	493	2	F75113	NADH dehydrogenase	225	76.5	5.5	548	2	B72542	glycerol kinase (E
153	78.5	5.6	579	2	A70954	hypothetical prote	226	76.5	5.5	725	2	S64124	probable cytochrom
154	78.5	5.6	622	2	E69609	hypothetical prote	227	76.5	5.5	746	2	T13698	probable membrane
155	78.5	5.6	624	2	T13814	cytochrome-c oxida	228	76.5	5.5	855	2	T47534	NADH2 dehydrogenas
156	78.5	5.6	732	2	T13814	peptide transporte	229	76.5	5.5	1187	2	T20544	hypothetical prote
157	78.5	5.6	744	2	T13485	NADH2 dehydrogenas	230	76.5	5.5	1342	2	E85614	hypothetical prote
158	78.5	5.6	1325	2	T01037	hypothetical prote	231	76.5	5.5	1342	2	G90750	cell division prot
159	78	5.6	158	2	T26519	hypothetical prote	232	76	5.5	261	2	A64066	probable metal-bin
160	78	5.6	307	2	D81082	conserved hypother	233	76	5.5	275	2	C97028	probable membrane
161	78	5.6	335	2	E81736	phospho-N-acetylmu	234	76	5.5	281	2	AB1585	B. subtilis yxkD p
162	78	5.6	382	2	E97742	hypothetical prote	235	76	5.5	282	2	D97767	hypothetical prote
163	78	5.6	388	2	G75375	hypothetical prote	236	76	5.5	336	2	T23902	hypothetical prote
164	78	5.6	396	2	AF0785	bicyclomycin resis	237	76	5.5	365	2	F82210	amino acid ABC tra
165	78	5.6	414	2	S53075	probable membrane	238	76	5.5	415	2	G83568	probable permease
166	78	5.6	422	2	H64489	hypothetical prote	239	76	5.5	447	2	C84306	hypothetical prote
167	78	5.6	462	2	T48661	acetate-CoA ligase	240	76	5.5	452	2	S46037	prephenate dehydro
168	78	5.6	688	2	T06299	potassium transpor	241	76	5.5	480	2	G83414	cytochrome-c oxida
169	78	5.6	701	2	T15238	hypothetical prote	242	76	5.5	502	2	JN0113	nicotinic acetylch
170	77.5	5.6	212	2	E83936	hypothetical prote	243	76	5.5	558	2	S08270	cytochrome-c oxida
171	77.5	5.6	283	2	H95887	probable ABC trans	244	76	5.5	578	2	T13664	NADH2 dehydrogenas
172	77.5	5.6	292	2	AD1182	sugar ABC transpor	245	76	5.5	617	2	T20409	hypothetical prote
173	77.5	5.6	293	2	AH0143	probable membrane	246	76	5.5	659	2	E85889	probable oxidoredu
174	77.5	5.6	296	2	C95326	AttA2-like ABC tra	247	76	5.5	659	2	B91045	probable oxidoredu
175	77.5	5.6	335	2	A72289	oligopeptide ABC t	248	76	5.5	669	1	DN0055	NADH2 dehydrogenas

395	73.5	5.3	674	2	E82954	conserved hypothet
396	73.5	5.3	699	2	T13730	NADH2 dehydrogenas
397	73.5	5.3	875	2	H90371	proteinase [import
398	73.5	5.3	885	2	B69783	transporter homolo
399	73.5	5.3	889	2	T20123	hypothetical prote
400	73.5	5.3	1099	2	A55405	adenylate cyclase
401	73.5	5.3	1128	2	T04922	hypothetical prote
402	73.5	5.3	1243	2	AF0611	cell division prot
403	73.5	5.3	2818	2	B55282	neurofibromatosis-
404	73.5	5.3	2820	2	JC5196	neurofibromin I -
405	73.5	5.3	2825	2	I54352	neurofibromin - mo
406	73	5.2	140	2	C83199	hypothetical prote
407	73	5.2	193	2	B91170	hypothetical membr
408	73	5.2	193	2	B86016	hypothetical prote
409	73	5.2	261	2	AC0251	high-affinity zinc
410	73	5.2	262	2	F97151	ABC transport MD
411	73	5.2	282	2	H71696	hypothetical prote
412	73	5.2	283	2	D83009	probable permease
413	73	5.2	292	2	C95147	licB protein [limp
414	73	5.2	294	2	D81434	probable 4-hydroxy
415	73	5.2	296	2	A98015	hypothetical prote
416	73	5.2	301	2	AH2064	hypothetical prote
417	73	5.2	311	2	T33436	hypothetical prote
418	73	5.2	364	2	D95959	conserved hypothet
419	73	5.2	384	2	S37608	NADH2 dehydrogenas
420	73	5.2	399	2	AE0396	probable sugar tra
421	73	5.2	401	2	T49929	hypothetical prote
422	73	5.2	436	2	S77639	exopolysaccharide
423	73	5.2	437	2	D86633	amino acid permeas
424	73	5.2	453	2	AD1556	conserved hypothet
425	73	5.2	456	2	H97735	hypothetical prote
426	73	5.2	470	2	B61118	transport of D-al
427	73	5.2	470	2	B91277	D-serine/D-alanine
428	73	5.2	470	2	S56432	D-serine/D-alanine
429	73	5.2	495	1	S25942	NADH2 dehydrogenas
430	73	5.2	507	2	AB1370	amino acid antipor
431	73	5.2	574	2	T05964	probable low-affin
432	73	5.2	633	2	T19189	hypothetical prote
433	73	5.2	639	2	G89839	protein C10C6.5 li
434	73	5.2	700	2	T13668	NADH2 dehydrogenas
435	73	5.2	732	2	T14233	NADH2 dehydrogenas
436	73	5.2	1564	2	T27121	hypothetical prote
437	73	5.2	3079	1	RGBY12	probable GTPase-ac
438	73	5.2	3898	1	GNMVHB	genome polyprotein
439	72.5	5.2	118	2	G64394	hypothetical prote
440	72.5	5.2	235	2	F95230	membrane protein l
441	72.5	5.2	235	2	A99095	conserved hypothet
442	72.5	5.2	235	2	AF0598	probable membrane
443	72.5	5.2	271	2	T11704	NADH2 dehydrogenas
444	72.5	5.2	284	2	AH0680	probable dimethyl
445	72.5	5.2	286	2	B99213	cytochrome C oxida
446	72.5	5.2	297	2	F82039	ribonuclease BN VC
447	72.5	5.2	308	2	AF0461	probable membrane
448	72.5	5.2	330	2	D95902	probable sugar ABC
449	72.5	5.2	347	2	AD2201	hypothetical prote
450	72.5	5.2	368	2	T13815	NADH2 dehydrogenas
451	72.5	5.2	375	2	B40205	Na+/H+-exchanging
452	72.5	5.2	421	2	T22969	hypothetical prote
453	72.5	5.2	434	2	D65132	hypothetical 46.5
454	72.5	5.2	458	2	B90623	NADH dehydrogenase
455	72.5	5.2	459	2	T19110	hypothetical prote
456	72.5	5.2	461	2	G85059	probable sugar tra
457	72.5	5.2	461	2	S75711	hypothetical prote
458	72.5	5.2	491	2	H83979	lysine decarboxyla
459	72.5	5.2	494	1	F69355	Na+/H+ antipor
460	72.5	5.2	498	2	B89832	hypothetical prote
461	72.5	5.2	523	2	AI1970	hypothetical prote
462	72.5	5.2	615	2	S77084	ABC-type transport
463	72.5	5.2	646	2	B70001	ABC transporter (p
464	72.5	5.2	682	2	T12715	NADH2 dehydrogenas
465	72.5	5.2	684	2	T13491	NADH2 dehydrogenas
466	72.5	5.2	704	2	T13665	NADH2 dehydrogenas
467	72.5	5.2	736	2	T12716	NADH2 dehydrogenas

468	72.5	5.2	741	2	T13085	NADH2 dehydrogenas
469	72.5	5.2	743	2	T13073	NADH2 dehydrogenas
470	72.5	5.2	744	2	T13040	NADH2 dehydrogenas
471	72.5	5.2	744	2	T13757	NADH2 dehydrogenas
472	72.5	5.2	917	2	T17244	hypothetical prote
473	72.5	5.2	923	2	C97487	hypothetical prote
474	72.5	5.2	923	2	AC2705	conserved hypothet
475	72.5	5.2	953	2	S54478	probable membrane
476	72.5	5.2	958	2	A70634	probable mmp11 pro
477	72.5	5.2	978	2	JC8067	mitochondrial Cl-t
478	72.5	5.2	1148	2	H90175	NADH dehydrogenase
479	72.5	5.2	1329	2	A64828	cell division prot
480	72.5	5.2	2658	2	A86216	protein T23G18.2 [
481	72	5.2	215	2	F75166	hypothetical prote
482	72	5.2	242	2	S49598	membrane protein -
483	72	5.2	249	2	A71234	hypothetical prote
484	72	5.2	252	2	A71165	hypothetical prote
485	72	5.2	257	2	AC1024	probable dimethyl
486	72	5.2	260	1	WMV2P0	FPO protein - fowl
487	72	5.2	261	2	S62047	probable membrane
488	72	5.2	282	2	D98058	hypothetical prote
489	72	5.2	286	2	D98058	hypothetical prote
490	72	5.2	315	2	B83778	hypothetical prote
491	72	5.2	339	2	E86761	ferrichrome ABC tr
492	72	5.2	339	2	T23244	conserved hypothet
493	72	5.2	355	2	A55733	G protein-coupled
494	72	5.2	359	2	AF3044	hypothetical prote
495	72	5.2	361	2	C84246	ribose ABC transpo
496	72	5.2	367	2	C82943	ferrichrome ABC tr
497	72	5.2	374	2	F98241	metL protein (AF00
498	72	5.2	378	2	T34372	hypothetical prote
499	72	5.2	417	2	F90916	probable transport
500	72	5.2	417	2	F64915	membrane protein Y
501	72	5.2	417	2	C85765	probable transport
502	72	5.2	421	2	B84129	ammonium transport
503	72	5.2	431	2	C82432	sugar transporter
504	72	5.2	440	2	C82410	conserved hypothet
505	72	5.2	440	2	T24076	nodulation protein
506	72	5.2	444	2	T24076	hypothetical prote
507	72	5.2	447	2	AE0094	probable gluconate
508	72	5.2	453	2	H71732	cytochrome D ubiqu
509	72	5.2	463	2	H69822	sodium-glutamate s
510	72	5.2	482	2	T17022	NADH2 dehydrogenas
511	72	5.2	507	2	B71695	NADH2 dehydrogenas
512	72	5.2	524	2	AD1897	hypothetical prote
513	72	5.2	530	1	G64918	adp, ATP carrier p
514	72	5.2	530	2	TS1836	phosphotransferase
515	72	5.2	582	2	H96604	high affinity nitr
516	72	5.2	582	2	AC2313	probable 3'-5' exo
517	72	5.2	602	2	AC2313	hypothetical prote
518	72	5.2	608	2	S76192	hypothetical prote
519	72	5.2	614	2	T13727	NADH2 dehydrogenas
520	72	5.2	620	2	F83976	cytochrome-c oxida
521	72	5.2	628	2	AG2707	hypothetical prote
522	72	5.2	629	2	H97489	mitochondrial tran
523	72	5.2	641	2	AG2164	hypothetical prote
524	72	5.2	644	2	B97885	transporter, trunc
525	72	5.2	681	2	T13566	NADH2 dehydrogenas
526	72	5.2	689	2	T11917	hypothetical prote
527	72	5.2	692	2	T33786	NADH2 dehydrogenas
528	72	5.2	698	2	T12565	NADH2 dehydrogenas
529	72	5.2	698	2	T12161	NADH2 dehydrogenas
530	72	5.2	700	2	T12161	NADH2 dehydrogenas
531	72	5.2	719	2	T13793	NADH2 dehydrogenas
532	72	5.2	796	2	S62464	conserved hypothet
533	72	5.2	906	2	S35312	coatomer complex b
534	72	5.2	2150	2	T08165	RNAi polyprotein -
535	71.5	5.1	213	2	A71049	hypothetical prote
536	71.5	5.1	232	2	E86825	hypothetical prote
537	71.5	5.1	260	2	H89899	phosphatidate cyti
538	71.5	5.1	281	2	A55862	aarA protein - Pro
539	71.5	5.1	281	2	B89769	hypothetical prote
540	71.5	5.1	285	2	AI1127	Staphylococcus xyl

541	71.5	5.1	295	2	AB0462	sn-glycerol-3-phos	614	71	5.1	468	2	D83625	probable transport
542	71.5	5.1	303	2	T32277	hypothetical prote	615	71	5.1	469	2	E86075	probable permease
543	71.5	5.1	308	2	H70767	hypothetical prote	616	71	5.1	478	2	A97079	MDR-type permease
544	71.5	5.1	323	2	G84003	DNA transport mach	617	71	5.1	492	2	D75188	proline symporter
545	71.5	5.1	324	2	F81018	iron(III) ABC tran	618	71	5.1	498	2	H81796	NADH2 dehydrogenas
546	71.5	5.1	337	2	F82214	galactoside ABC tr	619	71	5.1	502	1	ACHUA7	nicotinic acetylch
547	71.5	5.1	341	2	F82712	integral membrane	620	71	5.1	502	2	G02259	alpha 7 neuronal n
548	71.5	5.1	348	2	A82322	octaprenyl-diphosp	621	71	5.1	502	2	A57175	nicotinic acetylch
549	71.5	5.1	349	2	T31856	hypothetical prote	622	71	5.1	502	2	T01378	nicotinic receptor
550	71.5	5.1	349	2	A98094	type III secretion	623	71	5.1	509	2	A82840	beta-lactamase ind
551	71.5	5.1	373	2	E85939	hypothetical prote	624	71	5.1	541	2	D82302	iron(III) ABC tran
552	71.5	5.1	373	2	D71142	hypothetical prote	625	71	5.1	555	2	T24671	hypothetical prote
553	71.5	5.1	382	2	H85014	hypothetical prote	626	71	5.1	569	2	T00477	probable amino aci
554	71.5	5.1	391	2	A55119	potassium channel	627	71	5.1	579	2	AB1414	ABC transporter (A
555	71.5	5.1	406	2	C86904	transporter yxbD (628	71	5.1	593	2	A10559	probable ABC trans
556	71.5	5.1	418	2	H97763	proline/betaine tr	629	71	5.1	594	2	A49804	cellular Hsp70 hom
557	71.5	5.1	432	2	D95369	conserved hypotet	630	71	5.1	612	2	S74936	sulfur deprivation
558	71.5	5.1	445	2	T20190	hypothetical prote	631	71	5.1	684	2	T12151	NADH2 dehydrogenas
559	71.5	5.1	470	2	A69751	histidine permease	632	71	5.1	685	2	T12138	NADH2 dehydrogenas
560	71.5	5.1	470	2	C70554	hypothetical prote	633	71	5.1	686	2	T12128	NADH2 dehydrogenas
561	71.5	5.1	477	2	F86670	lysine specific pe	634	71	5.1	688	2	T13237	NADH2 dehydrogenas
562	71.5	5.1	497	2	G81598	serine hydroxymeth	635	71	5.1	688	2	T13249	NADH2 dehydrogenas
563	71.5	5.1	506	2	F88954	protein K04P1.14 (636	71	5.1	698	2	T12560	NADH2 dehydrogenas
564	71.5	5.1	512	2	S75887	hypothetical prote	637	71	5.1	699	2	T12648	NADH2 dehydrogenas
565	71.5	5.1	519	2	E86555	serine hydroxymeth	638	71	5.1	704	2	T13729	NADH2 dehydrogenas
566	71.5	5.1	519	2	H72067	glycine hydroxymet	639	71	5.1	737	2	T13067	NADH2 dehydrogenas
567	71.5	5.1	532	2	S59087	cytochrome-c oxida	640	71	5.1	918	2	A36337	membrane glycoprot
568	71.5	5.1	532	2	S66087	amino acid transpo	641	71	5.1	1506	2	T51900	related to PAN2 pr
569	71.5	5.1	533	2	H69326	conserved hypotet	642	70.5	5.1	133	2	A13582	hypothetical prote
570	71.5	5.1	534	2	C87023	probable cell divi	643	70.5	5.1	167	2	T20548	hypothetical prote
571	71.5	5.1	539	2	S77595	cytochrome-c oxida	644	70.5	5.1	175	2	T39999	hypothetical prote
572	71.5	5.1	654	2	H98871	hypothetical prote	645	70.5	5.1	210	2	F64609	conserved hypotet
573	71.5	5.1	663	2	AG2696	cytochrome c-type	646	70.5	5.1	214	2	S76538	hypothetical prote
574	71.5	5.1	663	2	G97478	cytochrome c-type	647	70.5	5.1	237	2	C64815	ybhM protein - Esc
575	71.5	5.1	685	2	B96668	probable acyl-CoA	648	70.5	5.1	253	2	F75067	hypothetical prote
576	71.5	5.1	672	2	AF3084	conserved hypotet	649	70.5	5.1	263	2	T29414	hypothetical prote
577	71.5	5.1	672	2	C98202	hypothetical prote	650	70.5	5.1	263	2	T04051	hypothetical prote
578	71.5	5.1	696	2	B87265	Kup system potassi	651	70.5	5.1	267	2	H72590	hypothetical prote
579	71.5	5.1	698	2	T12590	NADH2 dehydrogenas	652	70.5	5.1	285	2	T12435	probable plasma me
580	71.5	5.1	718	1	B64040	hypothetical prote	653	70.5	5.1	285	2	D87209	probable transmemb
581	71.5	5.1	730	2	T12224	NADH2 dehydrogenas	654	70.5	5.1	286	2	T02451	plasma membrane in
582	71.5	5.1	741	2	T12642	NADH2 dehydrogenas	655	70.5	5.1	288	2	S41194	transmembrane prot
583	71.5	5.1	741	2	T12701	NADH2 dehydrogenas	656	70.5	5.1	290	2	A69779	conserved hypotet
584	71.5	5.1	746	2	T13678	NADH2 dehydrogenas	657	70.5	5.1	297	2	G69357	hypothetical prote
585	71.5	5.1	756	2	T04187	subtilisin-like pr	658	70.5	5.1	312	2	AB0306	hypothetical prote
586	71.5	5.1	765	2	F97186	probable cell wall	659	70.5	5.1	315	1	C69763	ferrichrome ABC tr
587	71.5	5.1	770	2	T23999	hypothetical prote	660	70.5	5.1	315	2	C81962	probable inner mem
588	71.5	5.1	854	2	D82324	conserved hypotet	661	70.5	5.1	318	2	E71054	probable sodium de
589	71.5	5.1	1067	2	AB0260	probable phage hos	662	70.5	5.1	327	2	D75196	hypothetical prote
590	71.5	5.1	1679	2	T50091	yeast Ecm29 cell w	663	70.5	5.1	346	2	AB0187	probable iron-side
591	71	5.1	200	1	F45456	NADH2 dehydrogenas	664	70.5	5.1	349	2	T33948	hypothetical prote
592	71	5.1	228	2	AE2541	hypothetical prote	665	70.5	5.1	358	2	T22823	hypothetical prote
593	71	5.1	229	2	A64137	molybdenum transpo	666	70.5	5.1	386	2	E89765	branched chain ami
594	71	5.1	243	2	B86740	lipopolysaccharide	667	70.5	5.1	387	2	AE1062	hypothetical prote
595	71	5.1	260	2	T30669	probable trans-act	668	70.5	5.1	394	2	C81333	probable efflux pu
596	71	5.1	260	2	C82116	flagellar biosynth	669	70.5	5.1	408	2	B42290	probable membrane
597	71	5.1	261	2	H69217	hypothetical prote	670	70.5	5.1	419	2	B90033	hypothetical prote
598	71	5.1	272	2	T11689	NADH2 dehydrogenas	671	70.5	5.1	430	2	A95935	conserved hypotet
599	71	5.1	297	2	AD2318	transcription regu	672	70.5	5.1	434	2	T15799	hypothetical prote
600	71	5.1	305	2	E90461	hypothetical prote	673	70.5	5.1	443	2	D71058	hypothetical prote
601	71	5.1	316	2	AB2931	hypothetical prote	674	70.5	5.1	446	2	B99284	conserved hypotet
602	71	5.1	316	2	D98351	dipeptide ABC tran	675	70.5	5.1	457	2	A83677	sodium-dependent t
603	71	5.1	333	2	T41669	hypothetical prote	676	70.5	5.1	458	2	B90615	NADH dehydrogenase
604	71	5.1	364	2	H83787	hypothetical prote	677	70.5	5.1	474	2	T38737	probable CAAX pren
605	71	5.1	396	1	E64143	chloramphenicol re	678	70.5	5.1	480	2	S39978	scrA protein - Sta
606	71	5.1	397	2	C95221	hypothetical prote	679	70.5	5.1	491	2	AC1499	transmembrane prot
607	71	5.1	397	2	T00098	hypothetical prote	680	70.5	5.1	507	2	AB1707	glycine betaine tr
608	71	5.1	397	2	B98085	hypothetical prote	681	70.5	5.1	507	2	B64433	probable O-antigen
609	71	5.1	448	2	T30982	hypothetical prote	682	70.5	5.1	508	2	D81325	probable phosphate
610	71	5.1	458	2	AF0631	probable 4-hydroxy	683	70.5	5.1	533	2	S51171	amino acid transpo
611	71	5.1	461	2	S60253	sel-12 protein - C	684	70.5	5.1	585	2	C82955	probable sodium/pr
612	71	5.1	466	2	E90046	hypothetical prote	685	70.5	5.1	593	2	TJ0974	cytochrome-c oxida
613	71	5.1	468	2	I64182	Na+/H+-exchanging	686	70.5	5.1	593	2	F84223	cytochrome-c oxida

687	70.5	5.1	674	2	AC1913	two-component sens	760	70	5.0	2201	1	GNNYA9	genome polyprotein
688	70.5	5.1	683	2	T12158	NADH2 dehydrogenas	761	69.5	5.0	202	2	F86347	hypothetical prote
689	70.5	5.1	704	2	T13581	NADH2 dehydrogenas	762	69.5	5.0	210	2	H81406	probable integral
690	70.5	5.1	718	2	S48726	phenylalanine amio	763	69.5	5.0	215	2	S75345	hypothetical prote
692	70.5	5.1	733	2	T12213	NADH2 dehydrogenas	764	69.5	5.0	222	2	E72228	hypothetical prote
693	70.5	5.1	737	2	T13504	NADH2 dehydrogenas	765	69.5	5.0	224	2	B71191	hypothetical prote
694	70.5	5.1	738	2	C95936	conserved hypothet	766	69.5	5.0	256	2	S26742	topoplast intrinsi
695	70.5	5.1	740	1	DENTN5	NADH2 dehydrogenas	767	69.5	5.0	260	2	G64690	type IIS restricti
696	70.5	5.1	741	2	T12610	NADH2 dehydrogenas	768	69.5	5.0	265	2	AF2007	hypothetical prote
697	70.5	5.1	741	2	T12702	NADH2 dehydrogenas	769	69.5	5.0	268	2	A70417	hypothetical prote
698	70.5	5.1	741	2	T13233	NADH2 dehydrogenas	770	69.5	5.0	285	1	C32804	prephenate dehydra
699	70.5	5.1	741	2	T13569	NADH2 dehydrogenas	771	69.5	5.0	285	2	AE1488	Staphylococcus xyl
700	70.5	5.1	921	2	T19694	hypothetical prote	772	69.5	5.0	286	2	F87075	membrane transport
701	70.5	5.1	1134	2	A41350	adenylate cyclase	773	69.5	5.0	287	2	T09791	drought-induced ma
702	70.5	5.1	1881	2	A51338	sodium channel mNa	774	69.5	5.0	292	2	G75288	hypothetical prote
703	70.5	5.1	1781	1	A34374	DNA-directed RNA p	775	69.5	5.0	294	2	S76277	yef38 protein - Sy
704	70	5.0	98	2	G96595	hypothetical prote	776	69.5	5.0	308	2	S16648	dipeptide transport
705	70	5.0	160	2	F72322	NADH2 dehydrogenas	777	69.5	5.0	315	2	F72374	conserved hypothet
706	70	5.0	169	2	B72322	hypothetical prote	778	69.5	5.0	317	2	S72851	hypothetical prote
707	70	5.0	209	2	H97519	acetyltransferase	779	69.5	5.0	325	2	T14227	NADH2 dehydrogenas
708	70	5.0	240	1	Q0BEG3	hypothetical prote	780	69.5	5.0	329	2	T11350	NADH2 dehydrogenas
709	70	5.0	245	2	A90527	HMLF4 protein - hu	781	69.5	5.0	334	2	T19955	hypothetical prote
710	70	5.0	250	2	C91020	hypothetical prote	782	69.5	5.0	340	2	AE0353	probable membrane
711	70	5.0	251	2	AH0575	2,3-dihydro-2,3-di	783	69.5	5.0	351	2	T11794	NADH2 dehydrogenas
712	70	5.0	254	2	B70235	hypothetical prote	784	69.5	5.0	353	2	S65297	hypothetical prote
713	70	5.0	273	2	A72378	conserved hypothet	785	69.5	5.0	358	2	T29744	cytochrome c oxida
714	70	5.0	282	2	A93205	hypothetical prote	786	69.5	5.0	371	2	H97452	hypothetical prote
715	70	5.0	287	2	T12440	mipC protein - com	787	69.5	5.0	372	2	AE2717	permease [imported
716	70	5.0	320	2	T20176	hypothetical prote	788	69.5	5.0	385	2	S82790	permease AGR_C_211
717	70	5.0	325	2	C98135	hypothetical prote	789	69.5	5.0	385	2	H97498	nonstructural prot
718	70	5.0	325	2	AH3152	hypothetical prote	790	69.5	5.0	393	1	A48357	multidrug-efflux t
719	70	5.0	344	2	AE3228	agrocinopine synth	791	69.5	5.0	398	2	C90349	tryptophan transpo
720	70	5.0	344	2	S51948	hypothetical prote	792	69.5	5.0	415	2	A39412	hypothetical prote
721	70	5.0	345	2	H95381	probable iron uptra	793	69.5	5.0	420	2	A12458	phosphate permease
722	70	5.0	397	2	AF2016	hypothetical prote	794	69.5	5.0	426	2	E86575	branched-chain ami
723	70	5.0	413	2	H81659	branched-chain ami	795	69.5	5.0	439	2	A64769	phosphate permease
724	70	5.0	427	2	S74444	hypothetical prote	796	69.5	5.0	439	2	C90685	branched-chain ami
725	70	5.0	442	2	E85864	probable transport	797	69.5	5.0	439	2	G85535	NADH-ubiquinone/pl
726	70	5.0	443	2	H85485	probable transport	798	69.5	5.0	440	2	H90253	NADH-ubiquinone/pl
727	70	5.0	443	2	H90634	probable transport	799	69.5	5.0	443	2	AG1335	hypothetical prote
728	70	5.0	456	2	F97810	magnesium transport	800	69.5	5.0	448	2	A69747	ABC transporter (p
729	70	5.0	458	2	A37869	alpha-28-adrenergi	801	69.5	5.0	458	2	B81409	probable transmemb
730	70	5.0	459	2	T11110	NADH2 dehydrogenas	802	69.5	5.0	459	2	S10196	NADH2 dehydrogenas
731	70	5.0	459	2	S28025	light harvesting c	803	69.5	5.0	470	2	C87683	conserved hypothet
732	70	5.0	467	2	F91228	probable permease	804	69.5	5.0	472	2	B91091	L-arabinose isomer
733	70	5.0	503	2	AB2734	NADH dehydrogenase	805	69.5	5.0	472	2	E85936	L-arabinose isomer
734	70	5.0	503	2	D97515	NADH dehydrogenase	806	69.5	5.0	472	2	B26430	cytochrome-c oxida
735	70	5.0	519	2	F84222	quinone oxidoreduc	807	69.5	5.0	475	2	E83450	cytochrome-c oxida
736	70	5.0	522	2	B83987	ABC transporter (p	808	69.5	5.0	475	2	D83128	NADH2 dehydrogenas
737	70	5.0	539	2	E97025	spovB related memb	809	69.5	5.0	478	2	AC3395	NADH2 dehydrogenas
738	70	5.0	539	2	S67049	probable membrane	810	69.5	5.0	482	2	T45295	amino acid transpo
739	70	5.0	576	2	B71420	hypothetical prote	811	69.5	5.0	493	2	S52421	glycine betaine tr
740	70	5.0	600	2	T32343	hypothetical prote	812	69.5	5.0	507	2	T48645	glycine betaine tr
741	70	5.0	614	2	B84949	NADH2 dehydrogenas	813	69.5	5.0	507	2	AD1336	GRP-binding protei
742	70	5.0	658	2	B86599	metal transport p-	815	69.5	5.0	515	2	T03717	probable integral
743	70	5.0	658	2	D72026	metal transport p-	816	69.5	5.0	536	2	A71491	proline transport
744	70	5.0	670	2	QJ1447	NADH2 dehydrogenas	817	69.5	5.0	570	2	S04547	proline transport
745	70	5.0	683	2	C81515	cation-transportin	818	69.5	5.0	570	2	S04547	cytochrome-c oxida
746	70	5.0	688	2	T12670	NADH2 dehydrogenas	819	69.5	5.0	572	2	AE2671	NADH2 dehydrogenas
747	70	5.0	698	2	T12556	NADH2 dehydrogenas	820	69.5	5.0	591	2	S41115	hypothetical prote
748	70	5.0	700	2	T13702	NADH2 dehydrogenas	821	69.5	5.0	591	2	S43506	NADH2 dehydrogenas
749	70	5.0	705	2	T13494	NADH2 dehydrogenas	822	69.5	5.0	615	2	S77332	NADH2 dehydrogenas
750	70	5.0	732	2	T12194	NADH2 dehydrogenas	823	69.5	5.0	627	2	T11125	NADH2 dehydrogenas
751	70	5.0	738	2	T14230	NADH2 dehydrogenas	824	69.5	5.0	631	2	S67257	proline transport
752	70	5.0	744	2	AB1719	exodeoxyribonuclea	825	69.5	5.0	631	2	S75742	hypothetical prote
753	70	5.0	782	2	T25925	hypothetical prote	826	69.5	5.0	643	2	T70592	NADH2 dehydrogenas
754	70	5.0	836	2	E89453	protein F35H12.3 [827	69.5	5.0	654	2	T14202	NADH2 dehydrogenas
755	70	5.0	860	2	AB2044	adenylate cyclase	828	69.5	5.0	686	2	T13680	NADH2 dehydrogenas
756	70	5.0	1018	2	T19693	hypothetical prote	829	69.5	5.0	701	2	T12296	NADH2 dehydrogenas
757	70	5.0	1070	2	B86922	probable arabinosy	830	69.5	5.0	718	2	A99195	hypothetical prote
758	70	5.0	1155	2	B71720	hypothetical prote	831	69.5	5.0	736	2	T12214	NADH2 dehydrogenas
759	70	5.0	2108	2	S72458	sodium channel pro	832	69.5	5.0	741	2	T12706	NADH2 dehydrogenas
										741	2	T13086	NADH2 dehydrogenas

833	69.5	5.0	741	2	T13372	NADH2 dehydrogenas	906	69	5.0	670	1	DN0BU5	NADH2 dehydrogenas
834	69.5	5.0	744	2	T13682	NADH2 dehydrogenas	907	69	5.0	677	2	T11231	NADH2 dehydrogenas
835	69.5	5.0	747	2	E91049	probable cytochrom	908	69	5.0	684	2	T13695	NADH2 dehydrogenas
836	69.5	5.0	747	2	A85894	probable cytochrom	909	69	5.0	691	2	T12293	NADH2 dehydrogenas
837	69.5	5.0	809	1	SYBQ05	glutamine-CRNA lig	910	69	5.0	692	2	H71494	probable thiol-dis
838	69.5	5.0	870	2	A13605	potassium efflux s	911	69	5.0	702	2	T13505	NADH2 dehydrogenas
839	69.5	5.0	1302	2	B41249	multidrug resistanc	912	69	5.0	724	2	B83342	hypothetical prote
840	69.5	5.0	1645	2	T13339	carbamoyl-phosphat	913	69	5.0	737	2	T12193	NADH2 dehydrogenas
841	69.5	5.0	1827	2	A35694	cut1 protein - fis	914	69	5.0	777	2	AF2410	serine/threonine k
842	69.5	5.0	1828	2	T14455	cut1 protein - fis	915	69	5.0	903	2	A10015	maltose regulon p
843	69	5.0	139	2	T31033	hypothetical prote	916	69	5.0	904	2	A84212	hypothetical prote
844	69	5.0	171	2	AF2434	hypothetical prote	917	69	5.0	975	2	T22788	hypothetical prote
845	69	5.0	233	2	S77443	cytochrome-c oxida	918	68.5	4.9	179	2	AD2573	hypothetical prote
846	69	5.0	233	2	AH1068	probable membrane	919	68.5	4.9	212	2	AE1473	hypothetical prote
847	69	5.0	236	2	S42069	TEGT protein - rat	920	68.5	4.9	278	2	T11550	probable membrane
848	69	5.0	254	2	C84315	hypothetical prote	921	68.5	4.9	289	2	D87933	protein R06Cl.2 li
849	69	5.0	260	2	AG0434	probable membrane	922	68.5	4.9	295	2	T01528	probable plasma me
850	69	5.0	281	2	D64426	phosphate transpor	923	68.5	4.9	296	2	E69025	conserved hypot het
851	69	5.0	288	2	H72092	prolipoprotein dia	924	68.5	4.9	303	2	AG1396	cation transport p
852	69	5.0	288	2	G86529	prolipoprotein dia	925	68.5	4.9	305	2	S66005	conserved hypot het
853	69	5.0	290	2	T09260	aquaporin-like tra	926	68.5	4.9	313	2	C71545	probable oligopept
854	69	5.0	292	2	D81575	prolipoprotein dia	927	68.5	4.9	333	2	S52960	NADH2 dehydrogenas
855	69	5.0	296	1	BVSCPT	phosphate transpor	928	68.5	4.9	336	2	I64096	transmembrane pore
856	69	5.0	296	2	F91211	hypothetical prote	929	68.5	4.9	346	2	S98135	hypothetical prote
857	69	5.0	296	2	F86057	hypothetical prote	930	68.5	4.9	347	2	A13152	hypothetical prote
858	69	5.0	299	2	T06960	probable membrane	931	68.5	4.9	352	2	T23962	unknown protein F1
859	69	5.0	305	2	F70030	conserved hypot het	932	68.5	4.9	352	2	T23962	hypothetical prote
860	69	5.0	308	2	C86561	phosphatidate cyti	933	68.5	4.9	365	2	C97088	spore germination
861	69	5.0	308	2	H72062	conserved hypot het	934	68.5	4.9	367	2	T14228	NADH2 dehydrogenas
862	69	5.0	313	2	H71341	phosphatidate cyti	935	68.5	4.9	372	2	A80276	probable membrane
863	69	5.0	347	2	T29415	hypothetical prote	936	68.5	4.9	383	2	C83436	probable MFS metab
864	69	5.0	364	2	D96973	hypothetical prote	937	68.5	4.9	401	2	G95968	probable transport
865	69	5.0	369	2	F69478	spore germination	938	68.5	4.9	407	2	A69188	ammonium transport
866	69	5.0	387	2	E83679	NADH2 dehydrogenas	939	68.5	4.9	454	2	AE1244	acetyl-CoA carboxy
867	69	5.0	389	2	T51355	multidrug-efflux t	940	68.5	4.9	454	2	AE1244	acetyl-CoA carboxy
868	69	5.0	391	2	AB1285	membrane protein l	941	68.5	4.9	455	2	AE1244	acetyl-CoA carboxy
869	69	5.0	396	2	F83130	transmembrane tran	942	68.5	4.9	459	2	B95009	D-xylose-proton sy
870	69	5.0	397	2	E81223	probable MFS trans	943	68.5	4.9	459	2	B95009	potassium uptake p
871	69	5.0	397	2	B81994	conserved hypot het	944	68.5	4.9	459	2	F97880	hypothetical prote
872	69	5.0	411	2	F97088	probable transmemb	945	68.5	4.9	462	2	H81952	probable integral
873	69	5.0	416	2	C81324	sugar-proton sympo	946	68.5	4.9	468	2	AF2163	hypothetical prote
874	69	5.0	429	2	A10792	ubiquinol-cytochro	947	68.5	4.9	475	2	C33452	cytochrome-c oxida
875	69	5.0	431	2	A83380	probable transport	948	68.5	4.9	487	2	E37747	NADH2 dehydrogenas
876	69	5.0	432	2	C85087	hypothetical prote	949	68.5	4.9	488	1	QXASHI	NADH2 dehydrogenas
877	69	5.0	443	2	E64725	hypothetical prote	950	68.5	4.9	489	2	E89102	mRNA maturase bli
878	69	5.0	449	2	AE4707	YAU protein - Esc	951	68.5	4.9	507	2	B69316	protein F25E5.11 [
879	69	5.0	451	2	E81781	PTS system galacti	952	68.5	4.9	509	2	T41034	DNA gyrase, subuni
880	69	5.0	451	2	A81206	probable integral	953	68.5	4.9	537	2	A11277	probable WD-domain
881	69	5.0	455	2	B90619	probable integral	954	68.5	4.9	546	2	G86440	probable transport
882	69	5.0	458	2	B96643	sugar transporter,	955	68.5	4.9	546	2	G86440	hypothetical prote
883	69	5.0	462	2	D86814	NADH dehydrogenase	956	68.5	4.9	597	2	T41501	major facilitator
884	69	5.0	464	2	C40630	hypothetical prote	957	68.5	4.9	616	2	F90371	amino acid transpo
885	69	5.0	473	2	T03611	transport protein	958	68.5	4.9	627	2	C96981	ABC transporter AT
886	69	5.0	478	2	T29174	GDP-mannose pyroph	959	68.5	4.9	637	2	AC3217	ABC transporter AT
887	69	5.0	482	2	C90067	cyclin, B-type - c	960	68.5	4.9	637	2	AC3217	potassium uptake p
888	69	5.0	483	2	A81352	hypothetical prote	961	68.5	4.9	687	2	T12126	NADH2 dehydrogenas
889	69	5.0	487	2	S40820	hypothetical prote	962	68.5	4.9	688	2	T13242	NADH2 dehydrogenas
890	69	5.0	488	1	H64537	integral membrane	963	68.5	4.9	688	2	T13373	NADH2 dehydrogenas
891	69	5.0	488	2	G71969	probable permease	964	68.5	4.9	689	2	T13681	NADH2 dehydrogenas
892	69	5.0	492	2	AD3055	cytochrome-c oxida	965	68.5	4.9	698	2	T13492	NADH2 dehydrogenas
893	69	5.0	495	2	S75340	cytochrome-c oxida	966	68.5	4.9	701	2	F70155	Na+/H+ antiporter
894	69	5.0	498	2	H82494	succinoglycan bios	967	68.5	4.9	716	2	E82016	probable integral
895	69	5.0	509	2	D86978	NADH2 dehydrogenas	968	68.5	4.9	721	2	B83820	hypothetical prote
896	69	5.0	516	2	G82182	probable NADH dehy	969	68.5	4.9	736	2	T12225	NADH2 dehydrogenas
897	69	5.0	522	2	A98231	hypothetical prote	970	68.5	4.9	736	2	T12222	NADH2 dehydrogenas
898	69	5.0	528	2	T34941	probable NADH dehy	971	68.5	4.9	741	2	T12711	NADH2 dehydrogenas
899	69	5.0	554	2	S03809	succinoglycan bios	972	68.5	4.9	741	2	T12620	NADH2 dehydrogenas
900	69	5.0	588	2	A43740	probable Na+/H+ an	973	68.5	4.9	743	2	T13700	NADH2 dehydrogenas
901	69	5.0	591	2	G97748	cytochrome-c oxida	974	68.5	4.9	743	2	T12760	NADH2 dehydrogenas
902	69	5.0	605	2	H95240	virD4 protein [imp	975	68.5	4.9	744	2	T12705	NADH2 dehydrogenas
903	69	5.0	605	2	A93705	conserved hypot het	976	68.5	4.9	745	2	G84995	vacB protein [limp
904	69	5.0	642	2	T33262	hypothetical prote	977	68.5	4.9	746	2	C95110	competence protein
905	69	5.0	652	2	C97087	hypothetical prote	978	68.5	4.9	747	2	T13683	NADH2 dehydrogenas
						probable permease				750	2	B90137	sulfate permease l

979	68.5	4.9	820	2	D71471	probable DNA misma	1052	68	4.9	899	2	S76449	hypothetical prote
980	68.5	4.9	827	2	A95877	hypothetical prote	1053	68	4.9	906	2	S35342	Golgi-associated p
981	68.5	4.9	870	2	A83201	protein F32D8.4 li	1054	68	4.9	999	2	F72453	probable cytochrom
982	68.5	4.9	874	2	JQ0883	genome polypeptid	1055	68	4.9	1039	2	C87083	C-term lysyl-tRNA
983	68.5	4.9	881	2	AE2777	potassium efflux s	1056	68	4.9	1082	2	T45096	probable arabinosy
984	68.5	4.9	881	2	B97557	hypothetical prote	1057	68	4.9	1323	2	T18214	ATP binding casses
985	68.5	4.9	912	2	T21659	hypothetical prote	1058	68	4.9	1368	2	T51622	probable aldehyde
986	68.5	4.9	960	2	A82142	probable cell divi	1059	68	4.9	1541	1	S71839	canalicular multidi
987	68.5	4.9	1081	2	T52028	cellulose synthase	1060	67.5	4.8	100	2	B69836	hypothetical prote
988	68.5	4.9	1084	2	T08583	cellulose synthase	1061	67.5	4.8	212	2	A11111	hypothetical prote
989	68.5	4.9	1394	2	S66876	ATP-dependent tran	1062	67.5	4.8	269	2	E72693	hypothetical prote
990	68.5	4.9	1504	2	A33602	DNA-directed DNA p	1063	67.5	4.8	288	2	AC1198	Streptococcus agal
991	68	4.9	148	2	S74589	hypothetical prote	1064	67.5	4.8	284	2	T33224	hypothetical prote
992	68	4.9	183	2	T49855	hypothetical prote	1065	67.5	4.8	291	2	B95316	probable ABC trans
993	68	4.9	214	2	G83882	hypothetical prote	1066	67.5	4.8	293	2	D81673	ABC transporter, p
994	68	4.9	215	2	S16564	nolH protein - Rhi	1067	67.5	4.8	300	2	G70943	hypothetical prote
995	68	4.9	237	2	H86841	transport permease	1068	67.5	4.8	302	2	G90078	hypothetical prote
996	68	4.9	241	2	T33804	hypothetical prote	1069	67.5	4.8	302	2	F71660	hypothetical prote
997	68	4.9	252	2	A70529	hypothetical prote	1070	67.5	4.8	302	2	AF2686	ABC transporter, m
998	68	4.9	254	2	E70438	type 4 prepilin pe	1071	67.5	4.8	302	2	C97468	probable permease
999	68	4.9	256	2	C72261	spermidine/putresc	1072	67.5	4.8	304	2	AD1029	probable membrane
1000	68	4.9	265	2	AD0214	PTS system, mannos	1073	67.5	4.8	307	2	C70952	probable suga prot
1001	68	4.9	265	2	E82716	ATP synthase, A ch	1074	67.5	4.8	310	2	A86812	sugar ABC transpor
1002	68	4.9	282	2	AD0848	iron transport pro	1075	67.5	4.8	314	2	AE2230	hypothetical prote
1003	68	4.9	286	2	D83914	chloramphenicol re	1076	67.5	4.8	323	2	T31828	hypothetical prote
1004	68	4.9	296	2	AD0956	phosphate transpor	1077	67.5	4.8	327	1	S45529	NADPH2:quinone red
1005	68	4.9	304	2	A89905	hypothetical prote	1078	67.5	4.8	327	2	S67168	probable membrane
1006	68	4.9	312	2	F70044	hypothetical prote	1079	67.5	4.8	344	2	T32600	hypothetical prote
1007	68	4.9	316	2	S50336	hypothetical prote	1080	67.5	4.8	347	2	T28733	hypothetical prote
1008	68	4.9	316	2	E81321	probable cation tr	1081	67.5	4.8	349	2	S51267	probable galactosy
1009	68	4.9	329	2	F98334	SN-glycerol 3-phos	1082	67.5	4.8	359	2	I51372	angiotensin II rec
1010	68	4.9	335	2	S44635	f22b7.7 protein -	1083	67.5	4.8	361	2	D72384	conserved hypothet
1011	68	4.9	353	2	T06515	probable adenosylm	1084	67.5	4.8	364	1	S77360	cbiD protein - Syn
1012	68	4.9	357	2	C97744	hypothetical prote	1085	67.5	4.8	367	2	T23290	hypothetical prote
1013	68	4.9	358	2	T38914	para-hydroxybenzoa	1086	67.5	4.8	374	2	C51198	EspD protein limpo
1014	68	4.9	396	2	AF0677	probable membrane	1087	67.5	4.8	374	2	G86044	secreted protein E
1015	68	4.9	396	2	A91019	probable antibioti	1088	67.5	4.8	377	2	T21170	hypothetical prote
1016	68	4.9	396	2	C85863	probable antibioti	1089	67.5	4.8	379	2	D81515	cell shape-determi
1017	68	4.9	397	2	G90013	hypothetical prote	1090	67.5	4.8	387	2	JE0364	lactosylceramide a
1018	68	4.9	408	2	AC1373	conserved hypothet	1091	67.5	4.8	393	2	T12608	NADH2 dehydrogenas
1019	68	4.9	417	2	E82966	tryptophan permeas	1092	67.5	4.8	402	2	B69843	conserved hypothet
1020	68	4.9	437	1	F64614	conserved hypothet	1093	67.5	4.8	409	2	AF3271	probable allantoin
1021	68	4.9	442	2	H81402	probable integral	1094	67.5	4.8	415	2	F91209	low affinity trypt
1022	68	4.9	448	2	G70172	conserved hypothet	1095	67.5	4.8	415	2	A86056	low affinity trypt
1023	68	4.9	461	2	H82186	probable multidrug	1096	67.5	4.8	415	2	A86599	rod shape protein
1024	68	4.9	469	2	C69628	gamma-aminobutyrat	1097	67.5	4.8	415	2	C72026	rod shape protein
1025	68	4.9	476	2	D83600	probable aldehyde	1098	67.5	4.8	415	2	H71841	hypothetical prote
1026	68	4.9	485	2	T24115	hypothetical prote	1099	67.5	4.8	426	2	A86000	probable C4-dicarb
1027	68	4.9	488	1	QXASM4	NADH2 dehydrogenas	1100	67.5	4.8	456	2	E83750	gluconate permease
1028	68	4.9	489	2	B53153	glucose transport	1101	67.5	4.8	456	2	B83391	probable amino aci
1029	68	4.9	494	2	JC2382	sodium/proline sym	1102	67.5	4.8	459	2	S47879	NADH2 dehydrogenas
1030	68	4.9	505	2	B97747	NADH2 dehydrogenas	1103	67.5	4.8	462	2	D81010	conserved hypothet
1031	68	4.9	512	2	G90399	amino acid transpo	1104	67.5	4.8	463	2	A69905	conserved hypothet
1032	68	4.9	521	2	E64181	probable cytochrom	1105	67.5	4.8	463	2	E83242	probable adenylate
1033	68	4.9	523	2	T12198	sucrose transport	1106	67.5	4.8	467	2	AB2493	hypothetical prote
1034	68	4.9	534	2	S64593	probable membrane	1107	67.5	4.8	467	2	AB1263	probable integral
1035	68	4.9	537	2	AH1640	probable transport	1108	67.5	4.8	477	2	D83617	probable amino aci
1036	68	4.9	550	2	T37519	probable amino aci	1109	67.5	4.8	483	2	A10449	protein-Npi-phosph
1037	68	4.9	564	2	C83742	cytochrome c oxida	1110	67.5	4.8	486	2	F71683	NADH2 dehydrogenas
1038	68	4.9	592	2	E70488	cytochrome-c oxida	1111	67.5	4.8	490	2	E82740	C4-dicarboxylate t
1039	68	4.9	593	2	S26696	alkaline proteinas	1112	67.5	4.8	495	2	B81297	sodium/proline sym
1040	68	4.9	600	2	C69371	conserved hypothet	1113	67.5	4.8	501	2	T02134	hypothetical prote
1041	68	4.9	602	2	T13679	NADH2 dehydrogenas	1114	67.5	4.8	510	2	H87320	conserved hypothet
1042	68	4.9	617	2	F82744	ferrous iron trans	1115	67.5	4.8	512	2	S28663	cytochrome-c oxida
1043	68	4.9	633	2	I58140	glycine transporte	1116	67.5	4.8	513	2	I45456	NADH2 dehydrogenas
1044	68	4.9	633	2	S45877	uracil transport p	1117	67.5	4.8	514	2	T46131	4-coumarate-CoA li
1045	68	4.9	638	2	JH0673	glycine transport	1118	67.5	4.8	519	1	S02153	NADH2 dehydrogenas
1046	68	4.9	683	2	T12295	NADH2 dehydrogenas	1119	67.5	4.8	552	2	E70731	probable pitB prot
1047	68	4.9	688	2	T13378	NADH2 dehydrogenas	1120	67.5	4.8	560	2	F81423	L-lactate permease
1048	68	4.9	689	2	T13762	NADH2 dehydrogenas	1121	67.5	4.8	568	2	JC7911	Na+-coupled citrat
1049	68	4.9	705	2	T12152	NADH2 dehydrogenas	1122	67.5	4.8	615	2	H82635	hypothetical prote
1050	68	4.9	705	2	A97218	uncharacterized co	1123	67.5	4.8	617	2	B82285	proteoin-export mem
1051	68	4.9	811	2	T36581	probable transmemb	1124	67.5	4.8	631	2	H70754	probable abc trans

1271	66.5	4.8	261	2	I64249	hypothetical prote	1344	66.5	4.8	744	2	TI3063	NADH2 dehydrogenas
1272	66.5	4.8	269	2	A86889	zinc ABC transport	1345	66.5	4.8	744	2	TI3048	NADH2 dehydrogenas
1273	66.5	4.8	279	2	E69226	hypothetical prote	1346	66.5	4.8	746	2	TI0536	hypothetical prote
1274	66.5	4.8	292	2	A70546	probable menA prot	1347	66.5	4.8	755	2	T20950	hypothetical prote
1275	66.5	4.8	293	2	F83823	hypothetical prote	1348	66.5	4.8	759	2	D70422	cellulose synthase
1276	66.5	4.8	292	2	T41928	hypothetical prote	1349	66.5	4.8	790	2	G90477	hypothetical prote
1277	66.5	4.8	295	2	AE0993	glycerol-3-phospha	1350	66.5	4.8	812	2	TI6621	hypothetical prote
1278	66.5	4.8	306	2	C70141	oligopeptide ABC t	1351	66.5	4.8	820	2	T41978	helicase - human h
1279	66.5	4.8	306	2	S55047	ABC-type transport	1352	66.5	4.8	860	2	C92750	mannosyltransferas
1280	66.5	4.8	320	2	T23635	hypothetical prote	1353	66.5	4.8	919	2	SI9810	glutamate receptor
1281	66.5	4.8	361	2	T37938	hypothetical prote	1354	66.5	4.8	919	2	I53474	olfactory channel -
1282	66.5	4.8	362	2	G95376	conserved hypotet	1355	66.5	4.8	937	2	T37241	protein B0212.5 [i
1283	66.5	4.8	375	2	T05707	phosphate transpor	1356	66.5	4.8	957	2	D88651	hypothetical prote
1284	66.5	4.8	385	2	B87441	rod shape-determin	1357	66.5	4.8	999	2	T27628	conserved membrane
1285	66.5	4.8	389	2	AD3378	cell division prot	1358	66.5	4.8	1002	2	G97217	H+-exporting ATPas
1286	66.5	4.8	390	2	AH0260	conserved hypotet	1359	66.5	4.8	1010	1	PXZP2P	hypothetical prote
1287	66.5	4.8	394	2	TI3721	NADH2 dehydrogenas	1360	66.5	4.8	1049	2	T22762	B. subtilis yueB p
1288	66.5	4.8	405	2	T40193	hypothetical prote	1361	66.5	4.8	1068	2	AB1082	hypothetical prote
1289	66.5	4.8	409	2	B85735	probable membrane	1362	66.5	4.8	1088	2	H84604	probable cellulose
1290	66.5	4.8	410	2	E75290	probable multidrug	1363	66.5	4.8	1248	2	C98974	autolysin [impor
1291	66.5	4.8	411	2	S73218	preprotein translo	1364	66.5	4.8	1704	2	S71363	probable ATP-bindi
1292	66.5	4.8	421	2	E90883	hypothetical prote	1365	66.5	4.8	1704	2	A59188	ATP-binding cass
1293	66.5	4.8	422	2	H69839	multidrug resistan	1366	66	4.7	101	2	G69894	hypothetical prote
1294	66.5	4.8	428	2	G82918	hypothetical prote	1367	66	4.7	105	2	AH2209	hypothetical prote
1295	66.5	4.8	438	2	H91112	hypothetical prote	1368	66	4.7	158	2	S58016	probable olfactory
1296	66.5	4.8	438	2	H85957	partial probable t	1369	66	4.7	171	2	S44146	amis protein - Pse
1297	66.5	4.8	440	2	C71863	probable aminotran	1370	66	4.7	172	2	A83226	hypothetical prote
1298	66.5	4.8	441	2	TI9306	hypothetical prote	1371	66	4.7	195	1	CYHYAM	alpha-crystallin c
1299	66.5	4.8	452	2	D86835	maltose ABC transp	1372	66	4.7	203	2	AD2304	hypothetical prote
1300	66.5	4.8	454	2	A70079	conserved hypotet	1373	66	4.7	203	2	T05519	hypothetical prote
1301	66.5	4.8	467	2	F90544	conserved hypotet	1374	66	4.7	203	2	C85288	hypothetical prote
1302	66.5	4.8	467	2	TI6319	hypothetical prote	1375	66	4.7	204	2	D69097	hypothetical prote
1303	66.5	4.8	469	2	H76626	probable narK3 pro	1376	66	4.7	211	2	E89963	hypothetical prote
1304	66.5	4.8	471	2	F71543	probable dicarboxy	1377	66	4.7	255	2	AH0577	molybdopterin-cont
1305	66.5	4.8	472	2	E83497	probable amino aci	1378	66	4.7	256	2	JQ1106	conoplast intrinsi
1306	66.5	4.8	475	2	S07754	NADH2 dehydrogenas	1379	66	4.7	260	2	AG0904	probable membrane
1307	66.5	4.8	475	2	T46745	arginine/ornithine	1380	66	4.7	265	2	H90254	sulfate ABC transp
1308	66.5	4.8	478	2	D64895	probable membrane	1381	66	4.7	267	2	A87233	conserved membrane
1309	66.5	4.8	480	2	D90038	PTS system, sucros	1382	66	4.7	275	2	F83222	Nosy protein PA339
1310	66.5	4.8	484	2	E75138	osmoregulated prol	1383	66	4.7	276	2	B35252	hema concentration
1311	66.5	4.8	491	2	H84379	4-hydroxybutyrate	1384	66	4.7	280	2	F75057	hypothetical prote
1312	66.5	4.8	492	2	TI5603	hypothetical prote	1385	66	4.7	285	2	E84789	hypothetical prote
1313	66.5	4.8	498	2	AI0482	phosphate transpor	1386	66	4.7	285	2	D84789	plasma membrane in
1314	66.5	4.8	499	2	A65085	probable low-affin	1387	66	4.7	285	2	S44085	hypothetical prote
1315	66.5	4.8	509	2	TI1043	cytochrome-c oxida	1388	66	4.7	296	2	G72760	NADH2 dehydrogenas
1316	66.5	4.8	513	2	TI4864	probable monosacch	1389	66	4.7	298	2	TI3684	NADH2 dehydrogenas
1317	66.5	4.8	513	2	C81859	probable integral	1390	66	4.7	303	2	AB1772	cation transport p
1318	66.5	4.8	519	2	E90548	conserved hypotet	1391	66	4.7	307	2	TI6457	hypothetical prote
1319	66.5	4.8	520	2	D90014	hypothetical prote	1392	66	4.7	311	2	AI2697	permease [impor
1320	66.5	4.8	526	2	H85891	hydrogenase 4 memb	1393	66	4.7	311	2	B97480	hypothetical prote
1321	66.5	4.8	526	2	E65024	Hydrogenase-4 comp	1394	66	4.7	312	2	G69423	branched-chain ami
1322	66.5	4.8	530	2	TI1884	cytochrome-c oxida	1395	66	4.7	312	2	H90517	hypothetical prote
1323	66.5	4.8	553	2	T38541	probable sucrose c	1396	66	4.7	318	2	AI1811	hypothetical prote
1324	66.5	4.8	557	2	T49811	probable vacuolar	1397	66	4.7	320	2	T25308	NADH2 dehydrogenas
1325	66.5	4.8	569	2	T37706	probable sodium/hy	1398	66	4.7	322	2	TI3486	conserved hypotet
1326	66.5	4.8	573	2	T23102	hypothetical prote	1399	66	4.7	330	1	H69798	hypothetical prote
1327	66.5	4.8	574	2	G84578	probable potassium	1400	66	4.7	335	2	T39425	hypothetical prote
1328	66.5	4.8	648	2	C97961	DNA topoisomerase	1401	66	4.7	336	2	TI3762	hypothetical prote
1329	66.5	4.8	648	2	F95093	DNA gyrase chain B	1402	66	4.7	344	2	A83236	NADH2 dehydrogenas
1330	66.5	4.8	649	2	AB2154	hypothetical prote	1403	66	4.7	354	2	S70595	hypothetical prote
1331	66.5	4.8	659	2	S67175	probable membrane	1404	66	4.7	355	2	A64138	hypothetical prote
1332	66.5	4.8	660	1	S54746	cytochrome c-type	1405	66	4.7	357	2	T03557	hypothetical prote
1333	66.5	4.8	664	2	B53610	ntpi protein - Ent	1406	66	4.7	357	2	F81916	ribose transport s
1334	66.5	4.8	679	2	H95036	glycosyl hydrolase	1407	66	4.7	371	2	AD1201	probable integral
1335	66.5	4.8	699	2	TI2173	NADH2 dehydrogenas	1408	66	4.7	377	2	H64387	N-acyl-L-amino aci
1336	66.5	4.8	703	2	H86588	thio,disulfide int	1409	66	4.7	381	2	C71680	hypothetical prote
1337	66.5	4.8	703	2	H72034	thiol-disulfide in	1410	66	4.7	383	2	E87680	hypothetical prote
1338	66.5	4.8	714	2	G81503	thiol-disulfide in	1411	66	4.7	395	2	A86527	hypothetical prote
1339	66.5	4.8	725	2	S52990	phenylalanine ammo	1412	66	4.7	395	2	E72095	neutral amino acid
1340	66.5	4.8	732	2	AD0014	primosomal protein	1413	66	4.7	396	2	AH2859	MFS permease [impo
1341	66.5	4.8	737	2	D97907	alpha-xylosidase (1414	66	4.7	396	2	F97636	probable transport
1342	66.5	4.8	741	2	TI2605	NADH2 dehydrogenas	1415	66	4.7	398	2	H75043	mg2+ transport pro
1343	66.5	4.8	741	2	TI3361	NADH2 dehydrogenas	1416	66	4.7	404	2	S65991	membrane protein y

1417	66	4.7	408	2	B84591	hypothetical prote
1418	66	4.7	417	2	T13759	NADH2 dehydrogenas
1419	66	4.7	426	2	H71483	probable phosphate
1420	66	4.7	428	2	T25950	hypothetical prote
1421	66	4.7	430	2	G89962	hypothetical prote
1422	66	4.7	430	2	T45437	hypothetical prote
1423	66	4.7	431	2	S56228	alpha-factor recep
1424	66	4.7	436	2	T36432	probable transmemb
1425	66	4.7	442	2	D64995	hypothetical prote
1426	66	4.7	446	2	S60180	branched-chain ami
1427	66	4.7	449	2	AH1336	PTS system galacti
1428	66	4.7	449	2	H70546	hypothetical prote
1429	66	4.7	451	2	E96763	unknown protein F2
1430	66	4.7	460	2	H83264	probable transport
1431	66	4.7	472	1	S76266	hypothetical prote
1432	66	4.7	474	2	D69400	pantothenate perme
1433	66	4.7	480	2	A12308	cytochrome D ubiqu
1434	66	4.7	484	2	S58868	G protein-coupled
1435	66	4.7	488	2	D64108	glucuronate transpor
1436	66	4.7	489	2	G90422	sugar transport pr
1437	66	4.7	492	2	S41288	genome polyprotein
1438	66	4.7	495	2	T28717	hypothetical prote
1439	66	4.7	498	2	E81220	NADH2 dehydrogenas
1440	66	4.7	501	2	T11587	glucosyltransferas
1441	66	4.7	511	2	JH0173	alpha-bungarotoxin
1442	66	4.7	513	2	G96757	probable protein A
1443	66	4.7	515	2	T14239	NADH2 dehydrogenas
1444	66	4.7	515	2	T45552	cytochrome-c oxida
1445	66	4.7	549	1	A47468	cytochrome-c oxida
1446	66	4.7	585	2	AB2334	hypothetical prote
1447	66	4.7	579	2	A11789	ABC transporter (A
1448	66	4.7	581	2	T38501	hypothetical prote
1449	66	4.7	620	2	A53731	translation initia
1450	66	4.7	638	2	I77912	glycine transporte
1451	66	4.7	683	2	T12123	NADH2 dehydrogenas
1452	66	4.7	686	2	T13234	NADH2 dehydrogenas
1453	66	4.7	686	2	T13252	NADH2 dehydrogenas
1454	66	4.7	686	2	T13768	NADH2 dehydrogenas
1455	66	4.7	686	2	T13766	NADH2 dehydrogenas
1456	66	4.7	688	2	T13282	NADH2 dehydrogenas
1457	66	4.7	688	2	T13243	NADH2 dehydrogenas
1458	66	4.7	688	2	T13253	NADH2 dehydrogenas
1459	66	4.7	688	2	T13348	NADH2 dehydrogenas
1460	66	4.7	692	2	I57956	glycine transporte
1461	66	4.7	695	2	S70103	probable membrane
1462	66	4.7	696	2	T12659	NADH2 dehydrogenas
1463	66	4.7	698	2	T12563	NADH2 dehydrogenas
1464	66	4.7	700	2	T12589	NADH2 dehydrogenas
1465	66	4.7	702	2	T12624	NADH2 dehydrogenas
1466	66	4.7	723	2	T21869	hypothetical prote
1467	66	4.7	723	2	JC7795	epithelial calcium
1468	66	4.7	761	2	T14563	inorganic diphosph
1469	66	4.7	779	2	AH3125	GGDEF family prote
1470	66	4.7	780*	2	T22555	hypothetical prote
1471	66	4.7	890	2	B89047	protein C10G8.5 [l
1472	66	4.7	983	2	T19874	hypothetical prote
1473	66	4.7	1015	2	T15930	hypothetical prote
1474	66	4.7	1046	2	AD2959	AcrtB/AcrD/AcrF fam
1475	66	4.7	1046	2	B98324	probable rnd efflu
1476	66	4.7	1318	1	QOE1	membrane antigen p
1477	66	4.7	1318	2	S29606	P140 protein - hum
1478	66	4.7	1583	2	F97846	hypothetical prote
1479	66	4.7	1729	2	T43403	conserved hypothet
1480	66	4.7	2110	2	B44110	1,3-beta-glucan sy
1481	66	4.7	2191	2	T22345	hypothetical prote
1482	66	4.7	4377	2	A55575	ankyrin 3, long sp
1483	65.5	4.7	173	2	T23727	hypothetical prote
1484	65.5	4.7	179	2	D72360	conserved hypothet
1485	65.5	4.7	197	2	C84084	hypothetical prote
1486	65.5	4.7	205	2	T14046	hypothetical prote
1487	65.5	4.7	207	2	JX0142	cytochrome-c oxida
1488	65.5	4.7	219	2	S63393	probable membrane
1489	65.5	4.7	219	2	A86459	hypothetical prote

1490	65.5	4.7	227	2	T41464	probable Golgi men
1491	65.5	4.7	237	2	I38334	TEGR (testis enhan
1492	65.5	4.7	251	2	E72578	hypothetical prote
1493	65.5	4.7	261	2	F81376	probable integral
1494	65.5	4.7	262	2	G95320	NodJ membrane tran
1495	65.5	4.7	268	2	T22226	hypothetical prote
1496	65.5	4.7	271	2	E72202	conserved hypothet
1497	65.5	4.7	271	2	T41398	hypothetical prote
1498	65.5	4.7	273	1	T70127	gufa protein homol
1499	65.5	4.7	273	2	T06661	hypothetical prote
1500	65.5	4.7	277	2	T23276	hypothetical prote

ALIGNMENTS									
RESULT 1									
T13747									
hypothetical protein 22E5.9 - fruit fly (Drosophila melanogaster)									
C:Species: Drosophila melanogaster									
C>Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 31-Dec-2004									
C:Accession: T13747									
R:Murphy, L.; Harris, D.; Barrell, B.									
submitted to the EMBL Data Library, April 1999									
A:Description: Sequencing the distal X chromosome of Drosophila melanogaster.									
A:Reference number: Z17668									
A:Accession: T13747									
A:Status: preliminary; translated from GB/EMBL/DBJ									
A:Molecule type: DNA									
A:Residues: 1-246 <MUP>									
A:Cross-references: UNIPROT:O77262; UNIPARC:UPI000007747A; EMBL:AL031765; NID:									
C:Genetics:									
A:Cross-references: FlyBase:FBgn0000667									
A:Introns: 22/2; 63/1; 192/2									
A>Note: EG:22E5.9									
C:Superfamily: Caenorhabditis elegans hypothetical protein C36F7.4b									

Query Match	26.0%;	Score 361.5;	DB 2;	Length 246;
Best Local Similarity	33.6%;	Pred. No. 3.4e-24;		
Matches	78;	Conservative	50;	Mismatches 91; Indels 13; Gaps 4

QY	11	LPSALVIVTWSA	PFSVITATLTH	HIIDPALPYISD	TGTVAPKCLFG	AMLNIAAVLCIAT	70
Db	7	LPVLTFLIQV	TFLGTGTF	FAVLEGHVVPT	VPYISDAATY	SPSCVFGQLINIGSVLLGIT	66
QY	71	IYVRKYQVHAL	--SPB-ENVI	IKNKAGIVLGI	SLCGLSIVANF	OKTFLFAAHVSGAV	126
Db	67	IYVRQVQLQY	EHHPDLDSGL	RQNLALWFLG	VLVSLGSI	FGVNGQETNVRIVHIGAF	126
QY	127	LTFGMGSILYMF	QVITLSYQMP	KTHGKQVFW	IRLLVILWICG	VSALSML---TCSSVLHSG	183
Db	127	CCFGCGTLF	FMWQALISV	LIFPMSGTR	INAHRLGLMSV	CVCTILFILLAVTGVMSHILFKG	186
QY	184	NFGTDLEOKL	HWNPEDKGY	LVHLMITTAA	EHSMSPFS	PGFPFLTYIRDFOKISL	235
Db	187	-----QNP	RKWPSPDGGW	FHVVSSISEW	VIATVTFV	FFILSFETNEFRDVS	232

RESULT 2									
T19654									
hypothetical protein C33A11.2 - Caenorhabditis elegans									
C:Species: Caenorhabditis elegans									
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 31-Dec-2004									
C:Accession: T19654									
R:Gajadsky, S.									
submitted to the EMBL Data Library, August 1996									
A:Reference number: Z19158									
A:Accession: T19654									
A:Status: preliminary; translated from GB/EMBL/DBJ									
A:Molecule type: DNA									
A:Residues: 1-271 <WIL>									
A:Cross-references: UNIPROT:Q93319; UNIPARC:UPI0000080177; EMBL:Z79597; PIDN:C									
Experimental source: clone C33A11									

C:Genetics:
A:Gene: CESP:C33A11.2
A:Map position: X
A:Introns: 26/1; 117/3; 177/1; 208/3
C:Superfamily: Caenorhabditis elegans hypothetical protein C36F7.4b

Query Match 20.7%; Score 288; DB 2; Length 271;
Best Local Similarity 30.9%; Pred. No. 18-17; Mismatches 104; Indels 12; Gaps 6;
Matches 71; Conservative 43

QY 14 ALVITMSAAFIYSITAVTLHIDPALPYISDTGTVAPEKCLFGAMLNIAAVALCIATIVY 73
DB 18 ALIFFVQSFEV--YITAVLKHVDVPIFPVYLSAADKRQSCIFAIGANISSVLLALWV 75

QY 74 RYKQVHALSP--EENVIIKLNKAGLVGLSCIGLSIVANFQKTLFAAHVSGAVLTFQM 131
DB 76 RYRQLRGIFAFYDEANLQAWNRRQKWFVIAALGLFFVANVQETAIIIPVHMSAVASEGG 135

QY 132 GSILYMFVOTILSYQMPKIHGQVFWIRLLVW--CGVSALSM-LTCCSVLHSGNFGT 187
DB 136 FSYIMIFQCYLTHRVPTITLRTVYRIVFTIFSVCFCSCSGFGGIAASKIFHKTY--P 193

QY 188 DIEQLKHNPE--DKGYVLHMITTAAEWSMSFSFFGFFLTYYIRDFQKISL 235
DB 194 DLTPRPWRRIVQPGVELHQLSALAEMGCAISQIFFIQSFGPEFEDISL 243

RESULT 3
C88456
protein W03A5.2 [imported] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C:Accession: C88456
R:Anonymous, The C. elegans Sequencing Consortium.
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biology
A:Reference number: A75000; MUID:99069613; PMID:9851916
A:Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_ele
A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A:Accession: C88456
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-547 <STO>
A:Cross-references: UNIPARC:UPI000017A5D2; GB:chr.III; PIDN:AAA50731.1; PID:g485161; GSF
A:Note: weakly similar to gamma-glutamyl carboxylase
C:Genetics:
A:Gene: W03A5.2
A:Map position: 3

Query Match 8.6%; Score 120; DB 2; Length 547;
Best Local Similarity 21.8%; Pred. No. 0.01; Mismatches 100; Indels 26; Gaps 9;
Matches 48; Conservative 46

QY 51 PERCLFGAMLNIAAVALCIATIVYRVYKQVHALSPEEN---VIITKLNKAGLVGLSCIGLS 107
DB 14 PAKNAVYITNTHILLSSVMYLYKRELKSFRRQANISIIIFKGSRVNLFIGLAALTSYQ 73

QY 108 IVANFQKTLFAAHVSGAVLTFQMGSLYMFVQITLSYQMPKIHGQVFWIRLLVWCG 167
DB 74 LAVNFPATKINHVALLIGNKLALLANLYIWFHAFLSFKIR--DGNVPRMILFLIRI--- 127

QY 168 VSALSM-LTCCSVLHSGNFGDLSQKLHNPE-DKGYVLHMITTAAEWSMSFSFPFGFLTY 226
DB 128 --SLAFVVFV-----LGMNIQ-ANWVDPKQYL--AIDAIYEWCCYFAFCVFLITD 175

QY 227 IRDFQKISLR-VBANLHGLTYDT---APCPINNERTRLL 262
DB 176 AYEFRFMFRPKLIIRGCTGYNERVFPESCVDSEDEDNLT 215

RESULT 4
E69312
nitrate reductase gamma subunit homolog - Archaeoglobus fulgidus

C:Species: Archaeoglobus fulgidus
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C:Accession: E69312
R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A:Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Attiach, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo
A:Reference number: A69250; MUID:98049343; PMID:9389475
A:Accession: E69312
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-332 <KLE>
A:Cross-references: UNIPROT:O29749; UNIPARC:UPI00000570AA; GB:AE001069; GB:AE000782; NID

Query Match 7.4%; Score 103; DB 2; Length 332;
Best Local Similarity 17.0%; Pred. No. 0.18; Mismatches 112; Indels 60; Gaps 8;
Matches 45; Conservative 47

QY 2 WWFOQLSFL-----PSALVIWTSAAFIYSITAVTLHH---I 36
DB 65 WWETAGRMLEIFFRSLKKNTRYLDVRSQKDARWLMLFGILFHYSLLLVLRHRRFL 124

QY 37 DPALPYISDTGTVAPEKCLFGAMLNIAAVALCIATIVYRVYKQVHALSPEENVIILNKAGL 96
DB 125 DPVSFVETLSEIEAPKGVFIPSVYMGSLAIVAAFLMLRRIFLSRRTLSLPSDHFAL 184

QY 97 VLGILSCIGLSIVANFQKTLFAA-HVSGAVLTFQMGSLYMFVQITLSYQMPKIHGQV 155
DB 185 ILLLAITISGNVMRYFVKADLFAVKELLSMLMTFNIGHAVEVANTI-----BPI 233

QY 156 FWIRLLVWCGVSALSM-LTCCSVLHSG-----NFGTDLQKHL---WNPEDKGVYL 204
DB 234 FYVHPALASF---LLAYFPFSKLMHAGVFPSPTRNPNDRARRHNPDPADVPLIA 289

QY 205 HMITTAA-----EWSMSFSFF 220
DB 290 KGITVAGRVYKSKLDWDITYSMY 313

RESULT 5
A10561
integral membrane protein Aefa [imported] - Salmonella enterica subsp. enterica serovar
C:Species: Salmonella enterica subsp. enterica serovar Typhi
A:Title: this species has also been called Salmonella typhi
C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C:Accession: A10561
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
., S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.
A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A:Reference number: AB0502; MUID:21534947; PMID:11677608
A:Accession: A10561
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1120 <PAR>
A:Cross-references: UNIPARC:UPI000005A1F8; GB:AL513382; PIDN:CAD04963.1; PID:g16501750;
C:Genetics:
A:Gene: STY0522

Query Match 7.1%; Score 98.5; DB 2; Length 1120;
Best Local Similarity 19.5%; Pred. No. 1.6; Mismatches 101; Indels 93; Gaps 11;
Matches 58; Conservative 46

QY 1 WWWFOQLSFLPSALVIWTSAAFIYSITAVTLHIDPALPYISDTGTVAPEKCLFGAML 60
DB 805 MFW-----AIWSDLLTFSYLDLSITLWHYNG-----SEAGAAVVKSVTWMGSL 847

QY 61 -----NIAAVLCIATIVYRVYKQVHALSPEENVIILNKAGLVGLILS- 102

Db 848 FAIIAAMVAWALIRNLPGLLEVLVLSRLNMQGASVAITITILNYVIIAVGAMTVFGSLGV 907
Qy 103 -----CLGSIIVANFQKTTLFAAHVSGAVLTF-----GMGSLYMF 137
Db 908 SWDKLOMLAALAAVSGVGLQEIFGNFVSLGILIFRPVIRIGTWTVIGYSGTVSKIRIR 967
Qy 138 VOTILSYOMQPKIHGKQVFWIRLLLVIMCGVSALSMLTCSVLHSG-NFGTDLEQKLHWN 196
Db 968 ATTITDFRKEVIIPNKA-FVTERLINW-----SLSDTTTTLVIRLVGVAGSDLEK----- 1017
Qy 197 PEDKGVVLMHMTAA-----EWSMSFSPFGP-----FLTVIRDFQKISLRVE 238
Db 1018 -----VKRVLLQAAAMEHPKVMHDPPEPAVFFTFGASTLDHELRLYVRELRDSHTVD 1069

RESULT 6
E72523
carbon starvation protein A homolog APE2162 [similarity] - Aeropyrum pernix (strain K1)
C:Species: Aeropyrum pernix
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C:Accession: E72523
R:Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takahawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; KDNA Res. 6, 83-101, 1999
A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyrum pernix
A:Reference number: A72450; MUID:99310339; PMID:10382966
A:Accession: E72523
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-604 <RAW>
A:Cross-references: UNIPROT:Q9Y9X7; UNIPARC:UPI000005E231; DDBJ:AP000063; NID:G5105654;
A:Experimental source: strain K1
C:Genetics:
A:Gene: APE2162
C:Superfamily: carbon starvation protein

Query Match 7.0%; Score 97; DB 2; Length 604;
Best Local Similarity 23.9%; Pred. No. 1.1;
Matches 69; Conservative 39; Mismatches 101; Indels 80; Gaps 16;

Qy 4 FQOGLSFLPSAL--VWTSAAFIYSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAMLN 61
Db 183 YRMGLGMPSTVITVLLVIAAFVSYNHHGIVIGTFDPISLP-PQEGGWAYHRWVI--ILG 239
Qy 62 IAAVLICATIVYRYKQVHALSPEENVIIKLNAGLVLCGLSIVANFQKTTLFAAH 121
Db 240 LVALLA-ASLPVWY-----LLQPRD-----YLNAYILWTG-----LGLAAIA---AILIGTQS 283
Qy 122 VSGAVLTFMGSLYMFVQITLSYQMOPKIHGKQVFWIRLLLVIMCGVSALSMLTCSVLH 181
Db 284 LKGPAYT-----SFQPNIIAQPTP-----FWPAIPLIIACG-----SLSGFHSIVA 325
Qy 182 SGNFGYDLQKHL-----WN-PE--DKGYV-LHMITYA 210
Db 326 SGTTSKQLASELDALDFVGYGAMLEGALSGLAVIIPISPAWNAPELIQKGVIEENMLDLA 385
Qy 211 A-----EWSMSFSPFGPFLTVIRDFQKISLRVEANLHGLTYLDY 249
Db 386 AVPRYAVGYGYTLAKTFEMFGVGFDTGYGFFTLFASILMSLMYVLTLD 434

RESULT 7
S43882
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4 - garden lettuce mitochondrion
C:Species: Mitochondrion Lactuca sativa (garden lettuce)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C:Accession: S43882
R:Geier, K.T.; Abbas, G.M.; Makaroff, C.A.
Mol. Gen. Genet. 243, 97-105, 1994
A:Title: Intron loss from the NADH dehydrogenase subunit 4 gene of lettuce mitochondrion
A:Reference number: S43882; MUID:94247363; PMID:8190077
A:Accession: S43882

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-495 <GEI>
A:Cross-references: UNIPROT:Q37544; UNIPARC:UPI000008E589
C:Superfamily: NADH dehydrogenase (ubiquinone) chain 4
C:Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;

Query Match 6.9%; Score 96; DB 2; Length 495;
Best Local Similarity 24.6%; Pred. No. 1.1;
Matches 55; Conservative 34; Mismatches 83; Indels 52; Gaps 12;

Qy 8 LSFPLSALVWTSAAFIYSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAM--LNI--- 62
Db 277 LCFTP---FIYTLISAIAIYITSLTLRQID--LKKIIAYSSVAHMLNLTIGMFSLNIQGI 331
Qy 63 -----AAVLICATIVYRYKQ-----VHALSPEENVIIKLNAGLV 98
Db 332 GGSILLMLSHGLVSSALFLCVGLVIRKTRLVRYGGLVSTMPNFSTIFFFTLANMGL 391
Qy 99 -GILSCLG--LSIVANFQKTLFAAHVSGAVLTFMGSLYMFVQITLSYQMOP----- 148
Db 392 PGTSSFIGEFLLILVGAFQNSIVATLAALGMILGAAYSLWLY-NRVVSGNLKPDFLHKFS 450
Qy 149 KIHGKQVF-WTRLLI-VIWCVGVSALSMLTC-----SSVLHSGNF 185
Db 451 DLNGTEVFIFIPFLVGVVMGVYKVPDPCMHTSVSNLVQHGKF 494

RESULT 8
S16447
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4 - wheat mitochondrion
N:Alternate names: mitochondrial complex I subunit IV
C:Species: Mitochondrion Triticum aestivum (common wheat)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: S16447; S16448; S06835
R:Lamattina, L.; Grienenberger, J.M.
Nucleic Acids Res. 19, 3275-3282, 1991
A:Title: RNA editing of the transcript coding for subunit 4 of NADH dehydrogenase in wheat
A:Reference number: S16447; MUID:91288205; PMID:1712098
A:Accession: S16447
A:Molecule type: mRNA
A:Residues: 1-495 <LAW>
A:Cross-references: UNIPROT:P27572; UNIPARC:UPI00001720FA; EMBL:X57163
A:Note: The authors translated the codon CGT for residue 418 as Ala
A:Accession: S16448
A:Molecule type: DNA
A:Residues: 1-14, 'P', 16-24, 'TP', 27-35, 'P', 37-51, 'PP', 54, 'PR', 57-65, 'S', 67-105, 'S', 107-12
'H', 474-477, 'P', 479-495 <LAF>
A:Cross-references: UNIPARC:UPI000013079C; EMBL:X57164; NID:G21823; PIDN:CAA40453.1; PIC
A:Note: The authors translated the codon CGT for residue 418 as Ala
A:Note: 15-P, 25-Thr, 26-Pro, 36-Pro, 52-Pro, 53-Pro, 55-Pro, 56-Arg, 66-Ser, 106-Ser, 1
re due to RNA editing
R:Lamattina, L.; Weil, J.H.; Grienenberger, J.M.
FEBS Lett. 258, 79-83, 1989
A:Title: RNA editing at a splicing site of NADH dehydrogenase subunit IV gene transcript
A:Reference number: S06835; MUID:90076495; PMID:2687023
A:Accession: S06835
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 295-346 <LAW>
A:Cross-references: UNIPARC:UPI00001720FB
C:Genetics:
A:Gene: nad4
A:Genome: mitochondrion
A:Introns: 154/2; 326/1; 467/1
C:Superfamily: NADH dehydrogenase (ubiquinone) chain 4
C:Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;

Query Match 6.8%; Score 94; DB 1; Length 495;
Best Local Similarity 24.1%; Pred. No. 1.7;
Matches 54; Conservative 34; Mismatches 84; Indels 52; Gaps 11;

Qy 8 LSFPLSALVWTSAAFIYSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAM--LNI--- 62

Db 277 LCFTP---FIYTLAIAIYTSLTLRQID--LKIIAYSSVAHNMVLTIGMFSLNIOGI 331
QY 63 -----AAVLCIATYVRKYQ-----VHALSPENVIKLNKAGVLV 98
Db 332 GGSILLMLSHGLVSSALFLCVGLVYDRHKTRLVRYVGLVSTMPNFSTFFFTLANMSL 391
QY 99 -GILSCLG--LSIVANFOKTTLFAAHVSGAVLTFMGSLYMPVQTILSYQMOP----- 148
Db 392 PGTSGFIBGFLVLGAFOQNSLVATRALGMILGAAYSLWL-NRVSGNLKDPDFLYKFS 450
QY 149 KIHGKQVFWIR--LLLVWCGVSALSMLTC-----SSVLHSGNF 185
Db 451 DLNGREVFLFPLVGVWVGYPKVFELDCMHTSVSNLVQHGKF 494
RESULT 9
D96506
hypothetical protein T12C22.2 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: D96506
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.P.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; PMID:21016719; PMID:11130712
A:Accession: D96506
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-379 <STO>
A:Cross-references: UNIPROT:Q9LPP6; UNIPARC:UPI000000BFD0; GB:AE005173; NID:g8655985; PI
C:Genetics:
A:Gene: T12C22.2
A:Map position: 1
C:Superfamily: Arabidopsis thaliana hypothetical protein T9A21.70
Query Match 6.7%; Score 93.5; DB 2; Length 379;
Best Local Similarity 21.8%; Pred. No. 1.4;
Matches 47; Conservative 53; Mismatches 95; Indels 21; Gaps 9;
QY 10 FLPSALVIWTSAAFIYSYITAVTLHHIDPALPYISDTGTVAPEKCLFG-AMLNIAA---- 64
Db 90 YIP--LALLPSSASVESSESSCSLKYI--VLIYVLGVIIAGDNMLYSVGLLVLSASTYS 145
QY 65 VLCIATYVRKYQVHALSPENVIKLNKAGVLGILSCGLSIVANFOKTTLFAAHVSG 124
Db 146 LICATLAFNAVFSYFIPNAQKFTALILNSVLLSFSAAIALNDADPTSGVSRSKYIYG 205
QY 125 AVLTFCGSLYMPVQTILSYQMOPKIHGQVFWIRLLLVWCGVSALSMLTCSSVLHSGN 184
Db 206 FVCTLAASALYSLLSIMQFSFE-KILKRETSFVLEMQIYSLVA----TCVSVI--GL 258
QY 185 FGTDLEKQLHNPPE--DKG---YVLHMITTAEWSM 215
Db 259 FASGEWRTLHGEMEGYHKGQASVYLTVMTAVTWTQV 294
RESULT 10
F71651
putrescine-ornithine antiporter (potE) RP483 - Rickettsia prowazekii
C:Species: Rickettsia prowazekii
C:Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 05-Oct-2004
C:Accession: F71651
R:Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark, U
Nature 396, 133-140, 1998
A:Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria.

A:Reference number: A71630; MUID:99039499; PMID:9823893
A:Accession: F71651
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-429 <AND>
A:Cross-references: UNIPROT:Q9ZD63; UNIPARC:UPI000000D37BE; GB:AJ235269; NID
A:Experimental source: strain Madrid E
C:Genetics:
A:Gene: potE; RP483
C:Superfamily: ecotropic retrovirus receptor protein
Query Match 6.7%; Score 93.5; DB 2; Length 429;
Best Local Similarity 24.1%; Pred. No. 1.6;
Matches 48; Conservative 37; Mismatches 79; Indels 35; Gaps 10;
QY 11 LPSALVIWTSAAFIYSYITAVTLHHIDPA-----LPYISDTGTVAPEKCLFGMLN-- 61
Db 217 IPRAIIIGTCCVAFLYIINSIGIILIPASELINSKAPY-ADAATL-----LFGGTWRSK 270
QY 62 ---IAAVLCIATI---VVRKYQVHALSPENVIKLN-----NKAGVLGILSCIGLSIV 109
Db 271 ITVIASVICITLANVLTSCQIALGLAEDGLLPKFFAKKNSNNAPTYGIIISCLGITPL 330
QY 110 ANFOKTTLFAAHVSGAVLTFPMGSLYMPVQTILSYQMOPKI-HGKQVFWIRLLLVWCGV 168
Db 331 LLFTSNNAFAKQIT-QIIDFSV-TAFLFVYLICSLAFLKVFSSKENFSYYLF-----V 383
QY 169 SALSMLTCSSVLHSGNFC 187
Db 384 AIISIIPTCTWVIYKTPPET 402
RESULT 11
F90693
mechanosensitive channel protein [imported] - Escherichia coli (strain O157:H7, substrai
C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C:Accession: F90693
R:Hayaashi, T.; Makino, K.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gene
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: F90693
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1120 <HAY>
A:Cross-references: UNIPROT:Q8XD54; UNIPARC:UPI000000D03CB; GB:BA000007; PIDN:BA833941.1;
A:Experimental source: strain O157:H7, substrain RIMD 0509952
C:Genetics:
A:Gene: ECS0518
Query Match 6.7%; Score 93; DB 2; Length 1120;
Best Local Similarity 19.6%; Pred. No. 5;
Matches 46; Conservative 38; Mismatches 85; Indels 66; Gaps 8;
QY 1 MWVFOQGLSFLPSALVIWTSAAFIYSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAML 60
Db 805 MFW-----AIWSDLITVPSYLDLSITLHWYNG-----TEGAADVKNVTMGSL 847
QY 61 -----NIAAVLCIATYVRKYQVHALSPENVIKLNKAGVLGILS- 102
Db 848 FAIIASMVAVALLRNLPGLLEVLVLSRLNMRQASYAITTIILNYIIIAVGAMTVFGSLGV 907
QY 103 -----CLGLSIVANFOKTTLFAAHVSGAVLTF-----GMGSLYMF 137
Db 908 SMDKLQWLAAALSVGLGFLQEIFGNFVSGLLILFERPVRIGDVTTCGTSFSTVKIRIR 967
QY 138 VQTILSYQMOPKIHGKQVFWIRLLLVWCGVSALSMLTCSSVLHSG-NFGTDLEQ 191
Db 968 ATTITDFDRKEVLIIPKAF-VTERLINW----SLTDTTTLRILRVLGVAVGSDEK 1017

RESULT 12
B85544
mechanosensitive channel protein [similarity] - Escherichia coli (strain O157:H7, subsp. C); Species: Escherichia coli
C; Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C; Accession: B85544
R; Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A; Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A; Reference number: A85480; MUID:21074935; PMID:11206551
A; Accession: B85544
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-1120 <STO>
A; Cross-references: UNIPROT:O8XD54; UNIPARC:UPI00000D03CB; GB:AE0051174; NID:g12513332; E
A; Experimental source: strain O157:H7, substrain EDL933
C; Genetics:
A; Gene: aefa

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Best Local Similarity 19.6%; Pred. No. 5;
Matches 46; Conservative 38; Mismatches 85; Indels 66; Gaps 8;
QY 1 MWWFQGLSFLPSALVWTSAAFIYSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAML 60
Db 805 MFV-----AIWSDLITVFSYLDSTLWYNG-----TEAGAAVVKXNVVTGSL 847
QY 61 -----NTAAVLCIATYIVRYKQVHALSPENVIKLNKAGLVGLILS- 102
Db 848 FAIASMVAWALIRNLPGLLEVLVLSRLNMQGASVATITILNYIIIAVGAMTVFGSLGV 907
QY 103 -----CLGLSIVANFQKTLFAAHVSGAVLTF-----GMGSLYMP 137
Db 908 SWDKLOWLAALSVGLFGLOEIPGNFVSGLIILFERPVRIGTGTVIGSFSTVSKIR 967
QY 138 VOTILSYQMPKIHGKQVFWIRLLVIVCGVSALSMLTSCSSVLHSG-NFGTDLEQ 191
Db 968 ATTITDFRKEVIIPNKAFA-VTERLINW-----SLTDTTTLRLVIRLGVAAGSDLEK 1017
A; Title: The complete genome sequence of Escherichia coli K-12.
A; Reference number: A64720; MUID:97426617; PMID:9278503
A; Accession: H64776
A; Status: nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Residues: 1-1120 <BLAT>
A; Cross-references: UNIPROT:P77338; UNIPARC:UPI000012DD90; GB:AE000152; NID:9
A; Experimental source: strain K-12, substrain MG1655
C; Genetics:
A; Gene: aefa

C; Keywords: transmembrane protein
F; 12-28/Domain: transmembrane #status predicted <TM1>
F; 504-520/Domain: transmembrane #status predicted <TM2>
F; 561-577/Domain: transmembrane #status predicted <TM3>
F; 630-646/Domain: transmembrane #status predicted <TM4>
F; 663-679/Domain: transmembrane #status predicted <TM5>
F; 693-709/Domain: transmembrane #status predicted <TM6>
F; 793-809/Domain: transmembrane #status predicted <TM7>
F; 844-860/Domain: transmembrane #status predicted <TM8>
F; 892-908/Domain: transmembrane #status predicted <TM9>
Query Match 6.7%; Score 93; DB 2; Length 1120;
Best Local Similarity 19.6%; Pred. No. 5;

Matches 46; Conservative 38; Mismatches 85; Indels 66; Gaps 8;
QY 1 MWWFQGLSFLPSALVWTSAAFIYSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAML 60
Db 805 MFV-----AIWSDLITVFSYLDSTLWYNG-----TEAGAAVVKXNVVTGSL 847
QY 61 -----NTAAVLCIATYIVRYKQVHALSPENVIKLNKAGLVGLILS- 102
Db 848 FAIASMVAWALIRNLPGLLEVLVLSRLNMQGASVATITILNYIIIAVGAMTVFGSLGV 907
QY 103 -----CLGLSIVANFQKTLFAAHVSGAVLTF-----GMGSLYMP 137
Db 908 SWDKLOWLAALSVGLFGLOEIPGNFVSGLIILFERPVRIGTGTVIGSFSTVSKIR 967
QY 138 VOTILSYQMPKIHGKQVFWIRLLVIVCGVSALSMLTSCSSVLHSG-NFGTDLEQ 191
Db 968 ATTITDFRKEVIIPNKAFA-VTERLINW-----SLTDTTTLRLVIRLGVAAGSDLEK 1017

RESULT 14
AE0801
probable amino acid transporter STY2589 [imported] - Salmonella enterica subsp. enterica
C; Species: Salmonella enterica subsp. enterica serovar Typhi
A; Note: this species has also been called Salmonella typhi
C; Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C; Accession: AE0801
R; Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A; Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.,
A; Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A; Reference number: AE0502; MUID:21534947; PMID:11677608
A; Accession: AE0801
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-473 <PAR>
A; Cross-references: UNIPARC:UPI0000059B3D; GB:AL513382; PIDN:CAD07591.1; PID:g16503583;
C; Genetics:
A; Gene: STY2589

Query Match 6.6%; Score 92.5; DB 2; Length 473;
Best Local Similarity 22.8%; Pred. No. 2.2;
Matches 59; Conservative 36; Mismatches 95; Indels 69; Gaps 14;
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Db 37 SALLWVIAAPCLFFPLAWVCGELSTGWP--KGGIFWIKKAPKRIANIVVVCV---- 90
QY 73 VRYKQVHALSPENVIKLNKAGLVGLILSCLGLSIVANFQKTLFAAHVSGAVLT--- 128
Db 91 -----LFSCVLPFFPLMQFGFTAL--GYMIGGGLAENK 121
QY 129 --FGMGSLYMP-VQITLSYQMPKIHGKQVFWIRLL-LVIVCGV---SALSMLTSCSSVL 180
Db 122 AFIGIGSIVIFWLLTLMN-----IRGME--WTKIINSISAWCGVFIPIFSAILLAVVWL 173
QY 181 HSGN-FGTDLEQKLANPEDKGYVLHMITTAAEWSMSFSGFFELTYI-----RDF 230
Db 174 CTGHQMQDITYTAKNWP-DLG---HWDITVPLSSMMFAFAGLEVAPMIAGTRPNQPDF 229
QY 231 QKISLRVEANLHGLTYDT 249
Db 230 PRAMAVSAIVGIYVGT 248

RESULT 15
T24487
hypothetical protein T05A1.1 - Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C; Accession: T24487
R; Lloyd, C.

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: August 28, 2006, 17:31:24 ; Search time 300 Seconds
(without alignments)
820.180 Million cell updates/sec

Title: US-10-006-867-2

Perfect score: 1392

Sequence: 1 MMWFOGSLFLPSALVIWTS.....YDTAPCPINNERLLSRDI 266

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : UniProt_7.2.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1392	100.0	266	Q6UX65_HUMAN	Q6ux65 homo sapien
2	1383	99.4	266	Q4VWF6_HUMAN	Q4vwf6 homo sapien
3	1295	93.0	266	Q3ZC48_BOVIN	Q3zc48 bos taurus
4	1245	89.4	267	Q9CR48_MOUSE	Q9cr48 m 10 days e
5	1236	88.8	267	Q5BK09_RAT	Q5bk09 rattus norv
6	1235	88.7	267	Q9D520_MOUSE	Q9d520 mus musculus
7	805.5	57.9	180	Q9DB35_MOUSE	Q9db35 mus musculus
8	764.5	54.9	180	Q6IQ10_BRARE	Q6iq10 brachydanio
9	725	52.1	136	Q8NBQ4_HUMAN	Q8nbq4 homo sapien
10	492.5	35.4	238	Q8N682_HUMAN	Q8n682 homo sapien
11	479.5	34.4	238	Q9DC58_MOUSE	Q9dc58 mus musculus
12	477.5	34.3	240	Q5XJL0_BRARE	Q5xjl0 brachydanio
13	476.5	34.2	240	Q5RGJ7_BRARE	Q5rgj7 brachydanio
14	473.5	34.0	239	Q5EAK8_XENTR	Q5eak8 xenopus tro
15	471.5	33.9	287	Q6NRS6_XENLA	Q6nr6 xenopus lae
16	439.5	31.6	238	Q8QB2_ONCMY	Q8qb2 oncorhynch
17	388.5	27.9	237	Q7QE61_ANOGA	Q7qe61 anopheles g
18	361.5	26.0	246	Q77262_DROME	Q77262 drosophila
19	332.5	23.9	267	Q5DAX3_SCHJA	Q5dax3 schistosoma
20	318.5	22.9	252	Q86F93_SCHJA	Q86f93 schistosoma
21	289.5	20.8	232	Q32PK2_BRARE	Q32pk2 brachydanio
22	288	20.7	271	Q93319_CABEL	Q93319 caenorhabdi
23	277	19.9	73	Q4T5B8_TETNG	Q4t5b8 tetraodon n
24	267.5	19.2	231	Q4V7T3_XENLA	Q4v7t3 xenopus lae
25	262	18.8	238	Q8R218_MOUSE	Q8r218 mus musculus
26	260	18.7	293	Q61P61_CAEBR	Q61p61 caenorhabdi
27	258.5	18.6	230	Q4V7T7_XENLA	Q4v7t7 xenopus lae
28	251.5	18.1	181	Q6XHF5_DROVA	Q6xhf5 drosophila
29	251	18.0	132	Q9NUN1_HUMAN	Q9nun1 homo sapien
30	248	17.8	257	Q5DGL6_SCHJA	Q5dgl6 schistosoma
31	247	17.7	132	Q5EA39_BOVIN	Q5ea39 bos taurus

32	240	17.2	132	Q78J26_MOUSE	Q78j26 mus musculus
33	203	14.6	249	Q8C8S3_MOUSE	Q8c8s3 mus musculus
34	201.5	14.5	271	Q6GPL4_XENLA	Q6gpl4 xenopus lae
35	191.5	13.8	257	Q6IQJ3_BRACHYDANIO	Q6iqj3 brachydanio
36	188.5	13.5	308	Q4SA40_TETNG	Q4sa40 tetraodon n
37	185.5	13.3	219	Q8P6P1_MOUSE	Q8p6p1 mus musculus
38	183.5	13.2	294	Q7SXX4_BRARE	Q7sxx4 brachydanio
39	174.5	12.5	243	Q5S9G4_DICDI	Q5s9g4 dictyosteli
40	172.5	12.4	243	Q86IK0_DICDI	Q86ik0 dictyosteli
41	161.5	11.6	123	Q8C9L9_MOUSE	Q8c9l9 mus musculus
42	160.5	11.5	271	Q86TGI_HUMAN	Q86tgi homo sapien
43	157.5	11.3	271	Q8QZES_RAT	Q8qzes rattus norv
44	153.5	11.0	760	Q4SKZ5_TETNG	Q4skz5 tetraodon n
45	151.5	10.9	271	Q91WN2_MOUSE	Q91wn2 mus musculus
46	150.5	10.8	243	Q86K17_DICDI	Q86k17 dictyosteli
47	147.5	10.6	251	Q556P1_DICDI	Q556p1 dictyosteli
48	133.5	9.6	233	Q4T6B7_TETNG	Q4t6b7 tetraodon n
49	125.5	9.0	147	Q3TL78_MOUSE	Q3tl78 mus musculus
50	121.5	8.7	241	Q23135_CABEL	Q23135 caenorhabdi
51	120.5	8.7	207	Q550K4_DICDI	Q550k4 dictyosteli
52	119.5	8.6	273	Q628C5_CAEBR	Q628c5 caenorhabdi
53	117.5	8.4	246	Q61U88_CAEBR	Q61u88 caenorhabdi
54	113	8.1	362	Q3S118_RALME	Q3s118 ralstonia m
55	112.5	8.1	252	Q9U3U7_CABEL	Q9u3j7 caenorhabdi
56	112	8.0	307	Q474C6_RALEJ	Q474c6 ralstonia e
57	110.5	7.9	193	Q5C7G1_SCHJA	Q5c7g1 schistosoma
58	107.5	7.7	435	Q7QJU9_ANOGA	Q7qju9 anopheles g
59	106.5	7.7	140	Q8K117_MOUSE	Q8k117 mus musculus
60	105.5	7.6	207	Q54K87_DICDI	Q54k87 dictyosteli
61	105.5	7.6	881	Q5HAJ2_EHRRW	Q5haj2 ehrlichia r
62	105	7.5	217	Q5NE86_FRATT	Q5ne86 francisella
63	104.5	7.5	229	Q2WMT5_CIOBE	Q2wmt5 clostridium
64	103	7.4	299	Q6CD85_YARLI	Q6cd85 yarrowia li
65	103	7.4	332	HMEC_ARCFU	Q6cd85 archaeoglob
66	103	7.4	643	Q55R58_CRYNE	Q55r58 cryptococcus
67	103	7.4	643	Q5KGB1_CRYNE	Q5kg81 cryptococcus
68	101.5	7.3	255	Q9VPT7_DROME	Q9vpt7 drosophila
69	101.5	7.3	332	Q650W2_ORYSA	Q650w2 oryza sativ
70	101.5	7.3	881	Q5FG25_EHRRG	Q5fg25 ehrlichia r
71	101	7.3	218	Q8N2R6_HUMAN	Q8n2r6 homo sapien
72	101	7.3	293	Q55R99_MANSM	Q55r99 manheimia
73	101	7.3	495	N04M_ARATH	P93j13 arabidopsis
74	101	7.3	539	Q8EJE2_SHEON	Q8eje2 shewanella
75	100	7.2	347	Q46F94_METBA	Q46f94 methanosarc
76	99	7.1	305	Q3YR32_EHRCJ	Q3yr32 ehrlichia c
77	98.5	7.1	456	Q6D428_ERWCT	Q6d428 erwinia car
78	98.5	7.1	1120	Q5PFI4_SALPA	Q5pfi4 salmonella
79	98.5	7.1	1120	Q8ZRA5_SALTY	Q8zra5 salmonella
80	98.5	7.1	1120	Q8Z8T6_SALTI	Q8z8t6 salmonella
81	98.5	7.1	1140	Q57S86_SALCH	Q57s86 salmonella
82	98	7.0	495	Q6YSN0_BRANA	Q6ysn0 brassica na
83	98	7.0	495	Q8M8A9_BFTVU	Q8m8a9 beta vulgar
84	97.5	7.0	664	Q96D08_CABEL	Q96d08 caenorhabdi
85	97.5	7.0	746	Q9N5Q9_CABEL	Q9n5q9 caenorhabdi
86	97	7.0	382	Q38ZL6_LACSS	Q38zl6 lactobacill
87	97	7.0	390	Q8XQMO_RALSO	Q8xqmo ralstonia s
88	97	7.0	604	Q9Y9X7_AERPE	Q9y9x7 aeropyrum p
89	96.5	6.9	608	Q4HX42_GIBZE	Q4hx42 gibberella
90	96	6.9	369	Q38YX3_LACSS	Q38yx3 lactobacill
91	96	6.9	395	Q8EFB8_SHEON	Q8efb8 shewanella
92	96	6.9	460	Q3A8B8_PELAC	Q3a8b8 pelobacter
93	96	6.9	495	Q37544_LACSA	Q37544 lactuella sat
94	96	6.9	535	Q2ZBK9_9GAMM	Q2zbk9 shewanella
95	96	6.9	535	Q363W2_9GAMM	Q363w2 shewanella
96	96	6.9	535	Q36HJ6_9GAMM	Q36hj6 shewanella
97	96	6.9	572	Q4BVX0_CROWT	Q4bvxo crocospaer
98	96	6.9	615	Q7S1C6_NEUCL	Q7s1c6 neurospora
99	95.5	6.9	268	Q5WSU3_LEGPL	Q5wsu3 legionella
100	95.5	6.9	284	Q4ZW21_PSEUC	Q4zw21 pseudomonas
101	95.5	6.9	291	Q9ZFP3_ENTFC	Q9zfp3 enterococc
102	95.5	6.9	309	Q6NRD6_XENLA	Q6nrd6 xenopus lae
103	95.5	6.9	388	Q4PDR8_USTMA	Q4pd8 ustilego ma
104	95.5	6.9	486	Q8FQF5_COREF	Q8fqf5 corynebacte

105	95	6.8	440	2	Q4WU03 ASPFU	Q4wu03 aspergillus	178	90.5	6.5	614	2	Q9LNF0 ARATH	Q9lnf0 arabidopsis
106	95	6.8	599	2	Q38VM8_LACSS	Q38vm9 lactobacill	179	90.5	6.5	814	2	Q2ZY24_STRSU	Q2zy24 streptococc
107	95	6.8	702	2	Q9SC10_9MAGN	Q9sc10 tetracera a	180	90.5	6.5	1505	2	Q73JH5_TREDE	Q73jh5 treponema d
108	95	6.8	1120	2	Q32SD1_SHIBS	Q32sd1 shigella bo	181	90	6.5	281	2	Q54J51_DICDI	Q54j51 dictyosteli
109	94.5	6.8	229	2	Q4RR14_TETNG	Q4rr14 tetraodon n	182	90	6.5	283	2	Q8NUB1_CORGL	Q8nub1 corynebacte
110	94.5	6.8	268	2	Q5X117_LEGPA	Q5x117 legionella	183	90	6.5	396	2	Q8FFS3_ECOL6	Q8ffs3 escherichia
111	94.5	6.8	463	2	Q41CA9_9BACI	Q41ca9 exiguobacte	184	90	6.5	400	2	Q9KN80_VIBCH	Q9kn80 vibrio chol
112	94.5	6.8	469	2	Q7UF66_RHOBA	Q7uf66 rhodopirell	185	90	6.5	458	2	Q4S023_TETNG	Q4s023 tetraodon n
113	94.5	6.8	724	2	Q6FU10_CANGA	Q6fu10 candida gla	186	90	6.5	492	1	NU4M_CHOCR	NU4m chondrus cr
114	94	6.8	266	2	Q4FMG7_LEIMA	Q4fm77 leishmania	187	90	6.5	498	2	Q40PE9_DESAC	Q40pe9 desulfuroco
115	94	6.8	283	2	Q88MV8_PSEPK	Q88mv8 pseudomonas	188	90	6.5	505	2	Q5AEG5_CANAL	Q5aeg5 candida alb
116	94	6.8	452	2	Q5FI09_LACAC	Q5fi09 lactobacill	189	90	6.5	528	1	ATG22 YEAST	P25568 saccharomyc
117	94	6.8	495	1	NUAM_WHEAT	P27572 triticum ae	190	90	6.5	554	2	Q8GJF7_BDEBA	Q8gjf7 bdellovibri
118	94	6.8	542	2	Q3Q8S5_9GMM	Q3q8s5 shewanella	191	90	6.5	557	2	Q877D2_9CREN	Q877d2 pyrobaculum
119	94	6.8	543	2	Q3NIZ4_SHEFR	Q3niz4 shewanella	192	90	6.5	669	2	Q5A3N6_CANAL	Q5a3n6 candida alb
120	94	6.8	820	2	Q61KL4_CAEOR	Q61kl4 caenorhabdi	193	90	6.5	669	2	Q5A3V1_CANAL	Q5a3v1 candida alb
121	94	6.8	1120	2	Q8FK90_ECOL6	Q8fk90 escherichia	194	90	6.5	739	2	Q6MKW0_BDEBA	Q6mkw0 bdellovibri
122	93.5	6.7	303	2	Q2V417_ARATH	Q2v417 arabidopsis	195	89.5	6.4	270	2	Q886V4_PSESM	Q886v4 pseudomonas
123	93.5	6.7	367	2	Q3E7M0_ARATH	Q3e7m0 arabidopsis	196	89.5	6.4	360	2	Q30PV3_THIDN	Q30pv3 thiomicrosp
124	93.5	6.7	379	2	Q91PF6_ARATH	Q91pf6 arabidopsis	197	89.5	6.4	375	2	Q3CZL3_STRAG	Q3czl3 streptococc
125	93.5	6.7	429	2	Q9ZD63_RICPR	Q9zd63 rickettsia	198	89.5	6.4	437	2	Q9CL14_PASMU	Q9cl14 pasteurella
126	93.5	6.7	440	2	Q4QMF2_HAEIR	Q4qm2 haemophilus	199	89.5	6.4	440	1	DCUB_HAEIN	P44855 haemophilus
127	93.5	6.7	680	2	Q3G8W9_9FIRM	Q3g8w9 syntrophomo	200	89.5	6.4	440	2	Q65QD7_WANSM	Q65qd7 manheimia
128	93.5	6.7	1624	2	Q4I335_GIBZE	Q4i335 gibberella	201	89.5	6.4	443	2	Q929T2_LISIN	Q929t2 listeria in
129	93	6.7	576	2	Q5ZSX8_LEGPH	Q5zxs8 legionella	202	89.5	6.4	445	2	Q4I2Y6_DESHA	Q4i2y6 desulfitoba
130	93	6.7	688	2	Q3ACS1_RHOPA	Q3acs1 rhodopseudo	203	89.5	6.4	473	2	Q57L25_SALCH	Q57l25 salmonella
131	93	6.7	797	2	Q4S58E_CAEEL	Q4s58e caenorhabdi	204	89.5	6.4	482	2	Q4V1G2_BACCZ	Q4v1g2 bacillus ce
132	93	6.7	1120	1	KEFA_ECOLI	P77338 escherichia	205	89.5	6.4	485	2	Q88T41_LACPL	Q88t41 lactobacill
133	93	6.7	1120	2	Q32J45_SHIDS	Q32j45 shigella dy	206	89.5	6.4	495	2	Q59121_PYRHO	Q59121 pyrococcus
134	93	6.7	1120	2	Q3Z4T4_SHISS	Q3z4t4 shigella so	207	89.5	6.4	511	2	Q44R91_CHLLI	Q44r91 chlorobium
135	93	6.7	1120	2	Q2MBW2_ECOLI	Q2mbw2 escherichia	208	89.5	6.4	521	2	Q5ZYI3_LEGPH	Q5zyi3 legionella
136	93	6.7	1120	2	Q8XD54_ECO57	Q8xd54 escherichia	209	89.5	6.4	527	2	Q35I37_9BRAD	Q35i37 bradyrhizob
137	93	6.7	1120	2	Q83SE8_SHIFL	Q83se8 shigella fl	210	89.5	6.4	579	2	Q3DAC9_STRAG	Q3dac9 streptococc
138	93	6.7	1264	2	Q6BT03_DEBHA	Q6bt03 debaryomyce	211	89.5	6.4	579	2	Q3DHF4_STRAG	Q3dhf4 streptococc
139	92.5	6.6	251	2	Q970A1_SULTO	Q970a1 sulfolobus	212	89.5	6.4	579	2	Q3DTN1_STRAG	Q3dtn1 streptococc
140	92.5	6.6	473	2	Q8ZNC5_SALTY	Q8znc5 salmonella	213	89.5	6.4	579	2	Q3K170_STRAI	Q3k170 streptococc
141	92.5	6.6	473	2	Q8ZS06_SALTI	Q8zs06 salmonella	214	89.5	6.4	579	2	Q8DZT0_STRAS	Q8dzt0 streptococc
142	92.5	6.6	479	2	Q6SGM5_9BACT	Q6sgm5 uncultured	215	89.5	6.4	579	2	Q8E5H7_STRAS	Q8e5h7 streptococc
143	92.5	6.6	538	2	Q33WQ9_9GAMM	Q33wq9 shewanella	216	89.5	6.4	599	2	Q22089_CAEEL	Q22089 caenorhabdi
144	92.5	6.6	634	2	Q5KSP7_9ECHI	Q5ksp7 shewanella	217	89.5	6.4	963	2	Q7R2T8_GIALA	Q7r2t8 giardia lam
145	92.5	6.6	1117	2	Q4KJF2_PSEF5	Q4kf2 pseudomonas	218	89.5	6.4	1132	2	Q3NPV4_SHEFR	Q3npv4 shewanella
146	92.5	6.6	977	2	Q6CX54_KLULA	Q6cx54 kluyveromyc	219	89	6.4	267	2	Q8BV59_MOUSE	Q8bv59 mus musculu
147	92	6.6	399	2	Q3P0W7_9GAMM	Q3p0w7 shewanella	220	89	6.4	290	2	Q812M6_BACCR	Q812m6 bacillus ce
148	92	6.6	434	2	Q7VN68_HAEDU	Q7vn68 haemophilus	221	89	6.4	290	2	Q72YR6_BACCI	Q72yr6 bacillus ce
149	92	6.6	449	2	Q2JYC6_RHLET	Q2jyc6 rhizobium e	222	89	6.4	293	2	Q377V6_RHOPA	Q377v6 rhodopseudo
150	92	6.6	454	2	Q513Q7_ENTHI	Q513q7 entamoeba h	223	89	6.4	318	2	Q3G9U1_9FIRM	Q3g9u1 syntrophomo
151	92	6.6	594	2	Q5V2N6_HALWA	Q5v2n6 haloarcula	224	89	6.4	360	2	Q2XDW3_PSEPU	Q2xdw3 pseudomonas
152	91.5	6.6	268	2	Q5ZRL1_LEGPH	Q5zrl1 legionella	225	89	6.4	428	2	Q66FK2_YERPS	Q66fk2 yersinia ps
153	91.5	6.6	279	2	Q3Y299_ENTFC	Q3y299 enterococcu	226	89	6.4	428	2	Q8ZJ45_YERPE	Q8zj45 yersinia pe
154	91.5	6.6	387	2	Q22188_CAEEL	Q22188 caenorhabdi	227	89	6.4	442	2	Q7MP35_VIBVY	Q7mp35 vibrio vuln
155	91.5	6.6	430	2	Q810L4_CAEEL	Q8i0l4 caenorhabdi	228	89	6.4	637	2	Q9H8H9_HUMAN	Q9h8h9 homo sapien
156	91.5	6.6	444	2	Q67EN8_CALSI	Q67en8 callinectes	229	89	6.4	659	2	Q7VUY3_BORPE	Q7vuy3 bordetella
157	91.5	6.6	447	2	Q5QZ24_IDILO	Q5qz24 idiomarina	230	89	6.4	660	2	Q7WBD6_BORPE	Q7wbd6 bordetella
158	91.5	6.6	477	2	Q5U6C1_BETVU	Q5u6c1 beta vulgar	231	89	6.4	757	2	Q9UFA2_HUMAN	Q9ufa2 homo sapien
159	91.5	6.6	495	2	Q9MF62_BETVU	Q9mf62 beta vulgar	232	89	6.4	917	2	Q9H698_HUMAN	Q9h698 homo sapien
160	91.5	6.6	530	2	Q8BW48_LACPL	Q8bw48 lactobacill	233	89	6.4	1011	2	Q96F81_HUMAN	Q96f81 homo sapien
161	91.5	6.6	712	1	POT1_AEATH	Q22397 arabidopsis	234	88.5	6.4	266	2	Q41XM4_AZOPY	Q41xm4 azotobacter
162	91.5	6.6	712	2	Q56YD6_ARATH	Q56ydc6 arabidopsis	235	88.5	6.4	279	2	Q4BVQ2_CROWT	Q4bvq2 crocospaer
163	91.5	6.6	732	2	Q9TJY8_9GENT	Q9tjy8 condominea	236	88.5	6.4	283	2	Q43QV3_SOLUS	Q43qv3 solibacter
164	91.5	6.6	793	2	Q3SIJ3_THIDA	Q3sij3 thibobacillu	237	88.5	6.4	361	1	MRAY_COXBU	Q83f26 coxiella bu
165	91.5	6.6	1085	2	Q7VQP9_BLOFCH	Q7vpq9 blochmannia	238	88.5	6.4	361	2	Q3QV33_SOLUS	Q3q3v33 legionella
166	91.5	6.6	1117	2	Q3KJ67_PSEPP	Q3kj67 pseudomonas	239	88.5	6.4	403	1	MRAY_LEGPA	Q55xu0 cryptococcu
167	91.5	6.6	1221	2	Q4Q6N2_LEIMA	Q4q6n2 leishmania	240	88.5	6.4	403	2	Q55XU0_CRYNE	Q55xu0 legionella
168	91	6.5	257	2	Q6HIW4_BACHK	Q6hiw4 bacillus th	241	88.5	6.4	430	2	Q9KM52_CRYNE	Q9km52 cryptococcu
169	91	6.5	262	2	Q4WC47_ASFPFU	Q4wc47 aspergillus	242	88.5	6.4	430	2	Q9V210_PYRAB	Q9v210 pyrococcus
170	91	6.5	340	2	Q5NLU5_ZYMFO	Q5nlu5 zymomonas m	243	88.5	6.4	672	2	Q2NV24_9CHLO	Q2nv24 dunaliella
171	91	6.5	372	2	Q8NXX5_STAAR	Q8nxx5 staphylococ	244	88.5	6.4	680	2	Q9SBY7_9ASTE	Q9sby7 valnia cape
172	91	6.5	552	2	Q7WNJ3_BORBR	Q7wnj3 bordetella	245	88.5	6.4	685	2	Q2S0C0_9SPHI	Q2s0c0 salinibacte
173	91	6.5	554	2	Q37EY9_RHOPA	Q37ey9 rhodopseudo	246	88.5	6.4	692	2	Q8M8V0_9ASTE	Q8m8v0 vahlia cape
174	90.5	6.5	311	2	Q6CLU8_KLULA	Q6clu8 kluyveromyc	247	88.5	6.4	731	2	Q9TJP3_9GENT	Q9tjp3 simria viri
175	90.5	6.5	337	2	Q4NLG6_9MICC	Q4nlg6 arthrobacte	248	88.5	6.4	732	2	Q9TJS2_9GENT	Q9tjs2 pentagonia
176	90.5	6.5	443	2	Q5JH08_PYRKO	Q5jh08 pyrococcus	249	88.5	6.4	807	2	Q5CZ47_CAEEL	Q5cz47 caenorhabdi
177	90.5	6.5	579	2	Q3DLK9_STRAG	Q3dlk9 streptococc	250	88.5	6.4	808	2	Q21453_CAEEL	Q21453 caenorhabdi

251	88.5	6.4	833	2	Q7USM4_RHOBA	Q7usm4 rhodopirell	324	87	6.2	596	2	Q43WI9_SOLUS	Q43wi9 solibacter
252	88.5	6.4	1057	2	Q3PW11_NITHA	Q3pw11 nitrobacter	325	87	6.2	613	2	Q9I4D1_PSEAE	Q9i4d1 pseudomonas
253	88	6.3	263	2	Q3A731_PELCD	Q3a731 pelobacter	326	87	6.2	928	2	Q9LEC9_SOLTU	Q9lec9 solanum tub
254	88	6.3	290	2	Q4WVA6_BACCE	Q4wva6 bacillus ce	327	86.5	6.2	261	2	Q4QLK2_HAEI8	Q4qlk2 haemophilus
255	88	6.3	290	2	Q632P0_BACCH	Q632p0 bacillus ce	328	86.5	6.2	301	2	Q970T4_SULTO	Q970t4 sulfolobus
256	88	6.3	290	2	Q6HC79_BACCH	Q6hc79 bacillus th	329	86.5	6.2	341	2	Q44MQ7_CHLLI	Q44mq7 chlorobium
257	88	6.3	290	2	Q81KE4_BACAN	Q81ke4 bacillus an	330	86.5	6.2	368	2	Q439R1_ENTFA	Q439r1 enterococcus
258	88	6.3	324	2	Q4SF91_TETNG	Q4sf91 tetraodon n	331	86.5	6.2	400	1	YCEI_BACSU	YCEI1 bacillus su
259	88	6.3	331	2	Q2RKU5_MOOTH	Q2rku5 moorella th	332	86.5	6.2	403	2	Q4WDR2_ASFPF	Q4wdr2 aspergillus
260	88	6.3	331	2	Q8ALP0_BACTN	Q8alp0 bacteroides	333	86.5	6.2	441	2	Q4SY26_TETNG	Q4sy26 tetraodon n
261	88	6.3	372	2	Q8R792_THETN	Q8r792 thermoaer	334	86.5	6.2	465	2	Q38SD3_TETNG	Q38sd3 tetraodon n
262	88	6.3	413	2	Q4ZTV4_PSEOL	Q4ztv4 pseudomonas	335	86.5	6.2	467	2	Q41Q04_FERAC	Q41q04 ferriplasma
263	88	6.3	500	2	Q9TCC1_NEPOL	Q9tcc1 nephroselm	336	86.5	6.2	544	2	Q4UCA2_THERA	Q4uca2 theileria a
264	88	6.3	512	2	Q4G9Q3_METBA	Q4g9q3 methanosarc	337	86.5	6.2	547	2	Q5L797_CHLAB	Q5l797 chlamydomo
265	88	6.3	524	2	Q4NGAL_9MICC	Q4ngal arthrobacte	338	86.5	6.2	547	2	Q6N8M3_RHOPA	Q6n8m3 rhodopseudo
266	88	6.3	530	2	Q37CM4_RHOPA	Q37cm4 rhodopseudo	339	86.5	6.2	549	2	Q4KDN8_PSEF5	Q4kdn8 pseudomonas
267	88	6.3	546	2	Q8EXP0_METMA	Q8exp0 methanosarc	340	86.5	6.2	557	2	Q8ZXC1_PYRAE	Q8zxc1 pyrobaculum
268	88	6.3	622	2	Q7S317_NEUCR	Q7s317 neurospora	341	86.5	6.2	583	2	Q4ERC2_LISMO	Q4erc2 listeria mo
269	88	6.3	660	2	Q7WMV6_BORBR	Q7wmv6 bordetella	342	86.5	6.2	583	2	Q8Y9B6_LISMO	Q8y9b6 listeria mo
270	88	6.3	661	2	Q7AF70_GEOSL	Q7af70 geobacter s	343	86.5	6.2	586	2	Q7ZV33_BRARE	Q7zv33 brachydanio
271	88	6.3	732	2	Q9TJPI_9GENT	Q9tjpi1 wartszewicz	344	86.5	6.2	659	2	Q8MGF7_9DIPS	Q8mgf7 valeriana j
272	88	6.3	787	2	Q6SHL0_9BACT	Q6shl0 uncultured	345	86.5	6.2	732	2	Q9TJV8_9GENT	Q9tjv8 chimarrhis
273	88	6.3	929	2	Q9LGC6_ORYSA	Q9lgc6 oryza sativ	346	86.5	6.2	770	2	Q9YCS4_AERPE	Q9ygs4 aeropyrum p
274	88	6.3	1165	1	ADCV6_CANFA	P30804 canis famli	347	86.5	6.2	1527	2	Q4UD84_THEAN	Q4ud84 theileria a
275	87.5	6.3	215	2	Q9D2W6_MOUSE	Q9d2w6 mus musculu	348	86	6.2	198	2	Q3EZX8_BACTI	Q3ezk8 bacillus th
276	87.5	6.3	233	1	Y117_BORBU	O5n1144 borrelia bu	349	86	6.2	229	2	Q3PRM4_NITHA	Q3prm4 nitrobacter
277	87.5	6.3	235	2	Q5NO68_ZYMO	O5n668 zymomonas m	350	86	6.2	233	2	Q662P5_BORGA	Q662p5 borrelia ga
278	87.5	6.3	284	2	Q48LM2_PSEL4	Q48lm2 pseudomonas	351	86	6.2	234	2	Q8R3W1_MOUSE	Q8r3w1 mus musculu
279	87.5	6.3	300	2	Q5OYH0_ENTHI	Q5oyh0 entamoeba h	352	86	6.2	254	2	Q5DBF3_SCHJA	Q5dbf3 schistosoma
280	87.5	6.3	342	2	Q3GGZ3_CHLVI	Q3gz23 prosthecoch	353	86	6.2	279	2	Q3NMX9_SHEFR	Q3nmx9 shewanella
281	87.5	6.3	361	1	MRAY_LEGPH	O5wti4 legionella	354	86	6.2	331	2	Q3GHP3_CHLVI	Q3ghp3 prosthecoch
282	87.5	6.3	361	1	MRAY_LEGPH	O5wti4 legionella	355	86	6.2	339	2	Q4IEC2_GIBZE	Q4iec2 gibberella
283	87.5	6.3	365	2	Q6KHR7_MYCOP	Q6khr7 mycoplasma	356	86	6.2	372	2	Q5HHA6_STAAC	Q5haa6 staphylococ
284	87.5	6.3	374	2	Q3FU92_9BURK	Q3fu92 rhodofera	357	86	6.2	372	2	Q6GAU7_STAAS	Q6gau7 staphylococ
285	87.5	6.3	427	2	Q4UL81_RICFE	Q4ul81 rickettsia	358	86	6.2	373	2	Q7A6G2_STAAN	Q7a6g2 staphylococ
286	87.5	6.3	429	2	Q6WFP9_RICTY	Q6wfp9 rickettsia	359	86	6.2	373	2	Q9SVB1_PYRAB	Q9svb1 staphylococ
287	87.5	6.3	429	2	Q9KRP3_VIECH	Q9krp3 vibrio chol	360	86	6.2	389	2	Q9V0C0_PYRAB	Q9v0c0 pyrococcus
288	87.5	6.3	453	1	SERC1_MOUSE	Q6qz18 mus musculu	361	86	6.2	396	1	BCR_ECOLI	BCR246 escherichia
289	87.5	6.3	453	2	Q642W5_9ANNE	Q642w5 clymenella	362	86	6.2	396	2	Q2MAQ9_ECOLI	Q2maq9 escherichia
290	87.5	6.3	453	2	Q3UZ93_MOUSE	Q3uz93 m 8 days em	363	86	6.2	396	2	Q32HY2_SHIDS	Q32hy2 shigella dy
291	87.5	6.3	453	2	Q7TNK0_RAT	Q7tnk0 rattus norv	364	86	6.2	444	2	Q36BY3_9GNMM	Q36by3 shewanella
292	87.5	6.3	456	2	Q6BQ78_DEBHA	Q6bq78 debaryomyce	365	86	6.2	494	2	Q7R5J8_GIADIA	Q7r5j8 giardia lam
293	87.5	6.3	473	2	Q5PN23_SALPA	O5pn23 salmonella	366	86	6.2	509	2	Q7R5J8_GIADIA	Q7r5j8 giardia lam
294	87.5	6.3	482	1	YFYG_BACSU	P54723 bacillus su	367	86	6.2	531	2	Q2IUB9_RHOPA	Q2iub9 rhodopseudo
295	87.5	6.3	521	2	Q5X8G4_LEGPA	O5x8g4 legionella	368	86	6.2	593	2	Q2JTV5_9CVAN	Q2jtv5 cyanobacter
296	87.5	6.3	530	2	Q8EMR7_OCRH	O8emr7 oceanobacil	369	86	6.2	667	2	Q8W9Q3_MSVVI	Q8w9q3 mesostigma
297	87.5	6.3	544	2	Q18061_CABEL	O18061 caenorhabdi	370	86	6.2	701	2	Q8HTM4_ACHTR	Q8htm4 achlys trip
298	87.5	6.3	547	2	Q824X5_CHLCV	Q824x5 chlamydomo	371	86	6.2	703	2	Q9LMM3_ARATH	Q9lmm3 arabidopsis
299	87.5	6.3	671	2	Q73WX6_MYCPA	Q73wx6 mycobacteri	372	86	6.2	725	2	P92949_ARATH	P92949 arabidopsis
300	87.5	6.3	732	2	Q9TJQ2_9GENT	Q9tjg2 rustia sple	373	86	6.2	841	1	MPRF_STAXY	MPRF367 staphylococ
301	87.5	6.3	737	2	Q7OBT7_ANOGA	Q7obt7 anopheles g	374	86	6.2	883	2	Q3YRC6_EHRCJ	Q3yrc6 ehrlichia c
302	87.5	6.3	833	2	Q4TSU6_CORJK	Q4tsu6 corynebacte	375	86	6.2	954	2	Q7VGA9_HELHP	Q7vga9 helicobacte
303	87.5	6.3	1687	2	Q6QI17_RAT	Q6qi17 rattus norv	376	86	6.2	1308	2	Q8T6H2_DICDI	Q8t6h2 dictyosteli
304	87	6.2	161	2	Q4S8L4_TETNG	Q4s8l4 tetraodon n	377	86	6.2	1328	2	Q54EK2_DICDI	Q54ek2 dictyosteli
305	87	6.2	257	2	Q4VOX1_BACCC	Q4vox1 bacillus ce	378	86	6.2	1463	2	Q5AVK4_EMENI	Q5avk4 aspergillus
306	87	6.2	261	2	Q7VLV2_HABDU	Q7vlv2 haemophilus	379	85.5	6.1	219	2	Q9CY24_MOUSE	Q9cy24 mus musculu
307	87	6.2	269	2	Q458S9_9BURK	Q458s9 burkholderi	380	85.5	6.1	219	2	Q9DBL7_MOUSE	Q9dbl7 mus musculu
308	87	6.2	269	2	Q4LR84_9BURK	Q4lr84 burkholderi	381	85.5	6.1	250	2	Q6CID8_KIULA	Q6cid8 myxococc
309	87	6.2	271	2	Q6FLI1_ACIAD	Q6fli1 acinetobact	382	85.5	6.1	261	2	Q9CP79_PASMU	Q9cp79 pasteurella
310	87	6.2	350	2	Q3H352_NOCARD	Q3h352 nocardioide	383	85.5	6.1	295	2	Q9K0I7_NEIMB	Q9k0i7 neisseria m
311	87	6.2	396	2	Q8X5A2_ECO57	Q8x5a2 escherichia	384	85.5	6.1	295	2	Q5FA38_NEIGI	Q5fa38 neisseria g
312	87	6.2	410	2	Q62BS8_BURMA	Q62bs8 burkholderi	385	85.5	6.1	296	2	Q669X3_YERPE	Q669x3 yersinia ps
313	87	6.2	410	2	Q631L0_BURPS	Q631l0 burkholderi	386	85.5	6.1	296	2	Q82F11_YERPE	Q82f11 yersinia pe
314	87	6.2	412	2	Q4J710_SULAC	Q4j710 sulfolobus	387	85.5	6.1	304	2	Q4QJK4_EHRCJ	Q4qjk4 ehrlichia c
315	87	6.2	418	2	Q2YHSS_9ENTR	Q2yhss kluyvera as	388	85.5	6.1	311	1	PAQR3_HUMAN	PAQR37 homo sapien
316	87	6.2	435	1	EXOO_RHIME	Q2yn28 rhizobium m	389	85.5	6.1	311	2	Q8TD9_LACPL	Q8td9 lactobacill
317	87	6.2	456	2	Q3F3X5_9BURK	Q3f3x5 burkholderi	390	85.5	6.1	329	2	Q96K55_HUMAN	Q96k55 homo sapien
318	87	6.2	475	2	Q3NN43_SHEFR	Q3nn43 shewanella	391	85.5	6.1	355	2	Q8TNX8_METAC	Q8tnx8 methanosarc
319	87	6.2	517	2	Q61HG9_CAEBR	Q6lbg9 caenorhabdi	392	85.5	6.1	399	2	Q75PY5_CAVPO	Q75py5 cavia porce
320	87	6.2	535	2	Q5WU59_LEGPL	Q5wa59 legionella	393	85.5	6.1	401	2	Q89KV1_BRAJA	Q89kv1 bradyrhizob
321	87	6.2	535	2	Q5XZE0_LEGPA	O5xze0 legionella	394	85.5	6.1	414	2	Q2XJ8_PSEPU	Q2xj8 pseudomonas
322	87	6.2	560	2	Q5AVA3_EMENI	Q5ava3 aspergillus	395	85.5	6.1	440	2	Q3EGA9_ACTSC	Q3ega9 actinobacil
323	87	6.2	592	2	Q3JF87_BURP1	Q3jf87 burkholderi	396	85.5	6.1	453	2	Q5R419_PONPY	Q5r419 pongo pygma

397	85.5	6.1	453	2	Q5R4G3_PONPY	Q5r4g3 pongo pygma	470	84.5	6.1	479	2	Q651L0_ORYSA	Q651l0 oryza sativ
398	85.5	6.1	470	2	Q47836_TETNG	Q4t836 tetraodon n	471	84.5	6.1	479	2	Q9WZ89_THEMA	Q9wz89 thermotoga
399	85.5	6.1	482	2	Q3CNC3_ALTAT	Q3cnc3 pseudalter	472	84.5	6.1	491	2	Q18154_CAEEL	Q18154 caenorhabdi
400	85.5	6.1	482	2	Q4S4Z6_TETNG	Q4s4z6 tetraodon n	473	84.5	6.1	515	2	Q3LN48_ARATH	Q3ln48 arabidopsis
401	85.5	6.1	484	2	Q3UH23_MOUSE	Q3uh23 m 14 days p	474	84.5	6.1	562	2	Q9FLI8_ARATH	Q9fl18 arabidopsis
402	85.5	6.1	496	2	Q5ZMS7_CHICK	Q5zms7 gallus gall	475	84.5	6.1	589	2	Q95ZT6_CAEEL	Q95zt6 caenorhabdi
403	85.5	6.1	497	2	Q2RZQ5_9SPHI	Q2rzo5 salinibacte	476	84.5	6.1	638	2	Q33749_ARBLI	Q33749 arabcia lix
404	85.5	6.1	498	2	Q21287_RECAM	Q21287 reclinomona	477	84.5	6.1	671	2	Q55T80_CRYNE	Q55t80 cryptococcu
405	85.5	6.1	521	2	Q8WUB5_HUMAN	Q8wub5 homo sapien	478	84.5	6.1	674	2	Q5KJ61_CRYNE	Q5k161 cryptococci
406	85.5	6.1	526	2	Q90X46_BRARE	Q90x46 brachydanio	479	84.5	6.1	702	2	Q9TLF1_9LAMI	Q9tlf1 lindenbergi
407	85.5	6.1	528	2	Q6A2J4_9LAMI	Q6a2j4 brandisia h	480	84.5	6.1	913	2	Q7UJ14_RHOBA	Q7uj14 rhodopirell
408	85.5	6.1	545	2	Q96JZ5_HUMAN	Q96jz5 homo sapien	481	84.5	6.1	1982	2	Q4Q897_LEIMA	Q4q897 leishmania
409	85.5	6.1	572	2	Q4XZG8_PLACH	Q4xzg8 plasmodium	482	84	6.0	172	2	Q9TA01_LAMFL	Q9ta01 lampetra fl
410	85.5	6.1	587	1	TM9S3_MOUSE	Q9et30 mus musculu	483	84	6.0	234	2	Q3UAR5_MOUSE	Q3uar5 mus musculu
411	85.5	6.1	589	1	TM9S3_HUMAN	Q9hd45 homo sapien	484	84	6.0	234	2	Q39N04_MOUSE	Q39n04 mus musculu
412	85.5	6.1	589	2	Q5T857_HUMAN	Q5tcb57 homo sapien	485	84	6.0	295	2	Q7YFS4_HYME	Q7yfs4 neivanyrnex
413	85.5	6.1	629	2	Q571B0_MOUSE	Q571b0 mus musculu	486	84	6.0	298	2	Q48ER6_PSE14	Q48er6 pseudomonas
414	85.5	6.1	682	2	Q83C62_COXBU	Q83c62 coxiella bu	487	84	6.0	318	2	Q97NY1_STRPN	Q97ny1 streptococc
415	85.5	6.1	695	2	Q2QN15_ORYSA	Q2qn15 oryza sativ	488	84	6.0	329	2	Q8U0A2_PYRFU	Q8u0a2 pyrococcus
416	85.5	6.1	696	2	Q9TIW8_9ASTE	Q9tiw8 phacelia ro	489	84	6.0	367	2	Q3DVG6_CHLAU	Q3dvg6 chloroflexu
417	85.5	6.1	703	2	Q9TLA5_9LAMI	Q9tla5 jaeminium me	490	84	6.0	388	2	Q2KX95_BORAV	Q2kx95 bordetella
418	85.5	6.1	851	2	Q6FUB9_CANGA	Q6fu89 candida gla	491	84	6.0	396	2	Q2JAA7_9ACTO	Q2jaa7 frankia sp.
419	85.5	6.1	999	2	Q93JY2_ERWCH	Q93jy2 erwinaia chr	492	84	6.0	403	2	Q7MUU1_PORGI	Q7muu1 porphyromon
420	85	6.1	257	2	Q3V7U0_GEOKA	Q3v7u0 geobacillus	493	84	6.0	408	2	Q83MR3_TROWT	Q83mr3 tropheryma
421	85	6.1	304	2	Q96U46_NEUCR	Q96u46 neurospora	494	84	6.0	408	2	Q83N96_TROW8	Q83n96 tropheryma
422	85	6.1	307	2	Q6P7C6_ACIAD	Q6p7c6 acinetobact	495	84	6.0	448	2	Q5YTA9_NOCFA	Q5yta9 nocardia fa
423	85	6.1	333	2	Q6KCC9_CYPCA	Q6kcc9 cyprinus ca	496	84	6.0	459	2	Q5Z9R6_ORYSA	Q5z9r6 oryza sativ
424	85	6.1	338	1	PSTC1_MYCBO	P0a629 mycobacteri	497	84	6.0	460	2	Q59186_PYRHO	Q59186 pyrococcus
425	85	6.1	338	1	PSTC1_MYCTU	P0a628 mycobacteri	498	84	6.0	464	2	Q518J3_ENTHI	Q518j3 entamoeba h
426	85	6.1	339	2	Q5L5M5_CHLAB	Q5l5m5 chlamydothi	499	84	6.0	465	2	Q4ZYM6_PSEU2	Q4zym6 pseudonella
427	85	6.1	355	2	Q4L476_STAHL	Q4l476 staphylococ	500	84	6.0	478	2	Q2X075_9GAMM	Q2x075 shewanella
428	85	6.1	361	1	MRAY_NITEU	Q82v86 nitromonona	501	84	6.0	478	2	Q22X65_SHEPU	Q22x65 shewanella
429	85	6.1	369	2	Q9N2T7_CAEEL	Q9n2t7 caenorhabdi	502	84	6.0	478	2	Q74F67_GESOL	Q74f67 geobacter s
430	85	6.1	419	2	Q8NRU3_CORGL	Q8nr3 corynebacte	503	84	6.0	498	2	Q4E7G9_9RICK	Q4e7g9 wolbachia e
431	85	6.1	423	2	Q2US59_ASPOR	Q2us59 aspergillus	504	84	6.0	510	2	Q33Q28_9GAMM	Q33q28 shewanella
432	85	6.1	427	2	Q7PKH1_ANOGA	Q7pkh1 anophales g	505	84	6.0	529	2	Q35C75_9BRAD	Q35c75 bradyrhizob
433	85	6.1	443	2	Q9CEP2_LACLA	Q9cep2 lactococcus	506	84	6.0	534	2	Q41L15_METBU	Q41l15 methanococ
434	85	6.1	453	1	CAX1B_ORYSA	Q5tkg3 oryza sativ	507	84	6.0	575	2	Q91642_PSEAE	Q91642 pseudomonas
435	85	6.1	462	2	Q96YE7_SUITO	Q96ye7 sulfolobus	508	84	6.0	587	2	Q48BL8_PSE14	Q48bl8 pseudomonas
436	85	6.1	469	2	Q4C4C5_CROWT	Q4c4c5 crocospaer	509	84	6.0	597	2	Q9KUM6_VIRCH	Q9kuw6 vibrio chol
437	85	6.1	478	2	Q3Q3R8_9GAMM	Q3q3r8 shewanella	510	84	6.0	599	2	Q61Z28_CAEBR	Q61z28 caenorhabdi
438	85	6.1	497	2	Q6B376_DEBHA	Q6b376 debaryomyce	511	84	6.0	602	2	Q5QS30_MACLA	Q5qs30 macroctis la
439	85	6.1	498	2	Q9QXP0_MOUSE	Q9qxp0 mus musculu	512	84	6.0	673	2	Q46RW6_RALEJ	Q46rw6 raietonia s
440	85	6.1	522	2	Q9B8X9_FASHE	Q9b8x9 fasciola he	513	84	6.0	679	2	Q511J8_ENTHI	Q511j8 entamoeba h
441	85	6.1	524	2	Q8U4T9_HALVO	Q8u4t9 halobacteri	514	84	6.0	736	2	Q518I7_ENTHI	Q518i7 entamoeba h
442	85	6.1	543	2	Q83NH2_TROW8	Q83nh2 tropheryma	515	84	6.0	769	2	Q9TJ81_9CENT	Q9tj81 paucidianth
443	85	6.1	543	2	Q83GL8_TROW8	Q83gl8 tropheryma	516	84	6.0	830	2	Q6C772_YARLI	Q6c772 yarrowia li
444	85	6.1	543	2	Q6XJH9_9ERIC	Q6xjh9 sideroxylon	517	84	6.0	935	2	Q9ZP04_TROMA	Q9zp04 tropaeolum
445	85	6.1	658	2	Q6XJ14_9ERIC	Q6xj14 sideroxylon	518	84	6.0	4083	1	DYHC_ASHGO	Q9cim7 ashbya goss
446	85	6.1	821	2	Q2P9E8_XANOR	Q2p9e8 xanthomonas	519	83.5	6.0	261	1	Y1086_HABIN	P45030 haemophilus
447	85	6.1	845	2	Q80Z08_MOUSE	Q80z08 mus musculu	520	83.5	6.0	295	2	Q9JTVJ1_NEIMA	Q9jtvj1 neisseria m
448	85	6.1	887	2	Q5H6R2_XANOR	Q5h6r2 xanthomonas	521	83.5	6.0	311	2	Q4R6X2_MACFA	Q4r6x2 macaca fasc
449	85	6.1	1166	1	ADCY6_FAT	Q00343 rattus norv	522	83.5	6.0	324	2	Q8XX91_RALSO	Q8xx91 ralstonia s
450	84.5	6.1	224	2	Q4T540_TETNG	Q4t540 tetraodon n	523	83.5	6.0	330	2	Q8AA46_BACTN	Q8aa46 bacteroides
451	84.5	6.1	269	2	Q837L9_ENTFA	Q837l9 enterococcu	524	83.5	6.0	333	2	Q8E4D6_STR3A	Q8e4d6 streptococ
452	84.5	6.1	283	2	Q65D18_BACLD	Q65d18 bacillus li	525	83.5	6.0	453	2	Q3MHV9_BOVIN	Q3mhv9 bos taurus
453	84.5	6.1	298	2	Q4COM7_CROWT	Q4com7 crocospaer	526	83.5	6.0	468	2	Q8XKY8_CLOPE	Q8xky8 clostridium
454	84.5	6.1	323	2	Q7MTX3_PHOLL	Q7mtx3 photorhabdi	527	83.5	6.0	480	2	Q5DYP6_VIBF1	Q5dyp6 vibrio fisc
455	84.5	6.1	333	2	Q3DMN2_STRAG	Q3dmn2 streptococ	528	83.5	6.0	481	2	Q4RQ81_TETNG	Q4rq81 tetraodon n
456	84.5	6.1	395	2	Q6ND83_RHOPH	Q6nd83 rhodopseudo	529	83.5	6.0	500	2	Q41JH6_METBU	Q41jh6 methanococc
457	84.5	6.1	401	2	Q2Y4J7_9ARCH	Q2y4j7 uncultured	530	83.5	6.0	509	2	Q81A95_CABEL	Q81a95 caenorhabdi
458	84.5	6.1	405	2	Q65PD5_BACLD	Q65pd5 bacillus li	531	83.5	6.0	521	1	YJBC_SCHPO	Q74949 schizosacch
459	84.5	6.1	408	2	Q7XB13_WHEAT	Q7xb13 triticum ae	532	83.5	6.0	521	2	Q875S7_SACKL	Q875s7 saccharomyc
460	84.5	6.1	419	2	Q5PI23_AZOSE	Q5pi23 azoarcus sp	533	83.5	6.0	531	2	Q83EA0_COXBU	Q83ea0 coxiella bu
461	84.5	6.1	429	2	Q7Q0F3_ANOGA	Q7q0f3 anopheles g	534	83.5	6.0	605	2	Q9L1F6_STRCO	Q9llf6 streptomyce
462	84.5	6.1	449	2	Q2TCQ8_9INSE	Q2tcq8 petrobolus b	535	83.5	6.0	638	1	NUSM_PARLI	P12776 paracentrot
463	84.5	6.1	453	1	SERC1_HUMAN	Q9rxn5 homo sapien	536	83.5	6.0	693	2	Q85GD2_9DIPS	Q85gd2 nardostachy
464	84.5	6.1	453	2	Q9RNK3_RH1ET	Q9rnk3 rhizobium e	537	83.5	6.0	735	2	Q4WCR6_ASPFU	Q4wcr6 aspergillus
465	84.5	6.1	461	2	Q5ZME5_CHICK	Q5zme5 gallus gall	538	83.5	6.0	735	2	Q9TJZ7_9ANTHE	Q9tjz7 anthosperru
466	84.5	6.1	463	2	Q66C42_YERPE	Q66c42 yersinia ps	539	83.5	6.0	743	2	Q8WH76_FORGESIA	Q8wh76 forgesia ra
467	84.5	6.1	463	2	Q82FW8_YERPE	Q82fw8 yersinia pe	540	83.5	6.0	976	2	Q6FKX5_CANGA	Q6fkx5 candida gla
468	84.5	6.1	466	2	Q35PJ6_9BRAD	Q35pj6 bradyrhizob	541	83.5	6.0	1829	2	Q86HD9_DICTDI	Q86hd9 dictyosteli
469	84.5	6.1	473	2	Q65N12_BACLD	Q65n12 bacillus li	542	83.5	6.0	1867	2	Q55IP7_DICTDI	Q55ip7 dictyosteli

543	83	6.0	234	2	Q3UBS2_MOUSE	Q3u8e2 mus musculus	616	82.5	5.9	669	2	Q3N287_9DELTA	Q3n287 syntrophoba
544	83	6.0	241	1	YL068_MIMIV	Q5upe7 mimivirus	617	82.5	5.9	671	2	Q75113_ASHGO	Q75113 ashbya goss
545	83	6.0	297	2	Q4KA95_PSEF5	Q4ka95 pseudomonas	618	82.5	5.9	680	2	Q8SL84_9DIPS	Q8sl84 valeriana j
546	83	6.0	305	2	Q8YWR6_ANASP	Q8ywr6 anabaena sp	619	82.5	5.9	680	2	Q70SP4_9LAMI	Q70sp4 limosella m
547	83	6.0	318	2	Q8DNJ4_STRR6	Q8dnj4 streptococc	620	82.5	5.9	704	2	Q9SCD0_9ERIC	Q9scd0 gustavia su
548	83	6.0	321	1	OR5V1_HUMAN	Q9ugf6 homo sapien	621	82.5	5.9	1121	2	Q4T7Y0_TETNG	Q4t7y0 tetraodon n
549	83	6.0	321	2	Q6NTB5_HUMAN	Q6ntb5 homo sapien	622	82.5	5.9	1363	2	Q7PPE3_ANOGA	Q7ppe3 anopheles g
550	83	6.0	321	2	Q5QI19_HUMAN	Q5sqi9 homo sapien	623	82.5	5.9	1457	2	Q9HCE0_HUMAN	Q9hce0 homo sapien
551	83	6.0	324	2	Q4X186_ASPTU	Q4x186 aspergillus	624	82	5.9	219	2	Q75250_HUMAN	Q75250 homo sapien
552	83	6.0	361	2	Q3N8Q8_9PROT	Q3n8q8 nitrosomona	625	82	5.9	240	2	Q8ST72_MYCCA	Q8st72 mycoplasma
553	83	6.0	387	2	Q4AJC9_9CHLB	Q4ajc9 chlorobium	626	82	5.9	267	2	Q88HZ3_PSEPK	Q88hz2 pseudomonas
554	83	6.0	395	2	Q2ZQNA_SHEPU	Q2zqn4 shewanella	627	82	5.9	299	1	T2R16_RAT	Q8jku0 rattus norv
555	83	6.0	395	2	Q3GF10_9GAMM	Q3gf10 shewanella	628	82	5.9	313	2	Q87GV0_VTBPA	Q87gv0 vibrio para
556	83	6.0	397	2	Q41BF8_9BACI	Q41bf8 exiguirobact	629	82	5.9	317	2	Q9K6Y6_BACHD	Q9k6y6 bacillus ha
557	83	6.0	427	2	Q7PBQ1_RICSI	Q7pbq1 rickettsia	630	82	5.9	327	2	Q9KT03_VTBCH	Q9kt03 vibrio chol
558	83	6.0	427	2	Q92HP5_RICCN	Q92hp5 rickettsia	631	82	5.9	339	2	Q84ET2_9PROC	Q84et2 uncultured
559	83	6.0	457	2	Q8ULE5_PYRFU	Q8ule5 pyrococcus	632	82	5.9	347	2	Q4IU66_AZOVI	Q4iu66 azotobacter
560	83	6.0	460	2	Q9VOY7_PYRAB	Q9voy7 pyrococcus	633	82	5.9	356	2	Q9FZ96_ARATH	Q9fz96 arabidopsis
561	83	6.0	466	2	Q7VNG8_HABDU	Q7vng8 haemophilus	634	82	5.9	356	2	Q9M7R1_ARATH	Q9m7r1 arabidopsis
562	83	6.0	467	2	Q6F9F8_ACIAD	Q6f9f8 acinetobact	635	82	5.9	359	2	Q97C50_THEVO	Q97c50 thermoplas
563	83	6.0	474	2	Q3GPF2_9GAMM	Q3gpf2 psychrobact	636	82	5.9	365	2	Q5M7L7_XENTR	Q5m7l7 xenopus tro
564	83	6.0	496	2	Q91418_PSRAR	Q91418 pseudomonas	637	82	5.9	389	2	Q25590_HELPI	Q25590 helicobacte
565	83	6.0	508	2	Q2TY23_ASPOR	Q2ty23 aspergillus	638	82	5.9	392	2	Q40GS4_9RHOB	Q40gs4 jannaschia
566	83	6.0	511	2	Q5V404_HALMA	Q5v404 haloarcula	639	82	5.9	395	2	Q35ZLI_9GAMM	Q35zli shewanella
567	83	6.0	554	2	Q8Y8N1_NITMU	Q2y8n1 nitrosospir	640	82	5.9	395	2	Q3Q6Y1_9GAMM	Q3q6y1 shewanella
568	83	6.0	537	2	Q8Y7Z8_PSESM	Q8y7z8 pseudomonas	641	82	5.9	405	2	Q983X3_RHILO	Q983x3 rhizobium l
569	83	6.0	587	1	NUSM_STRPU	P15552 strongyloce	642	82	5.9	412	2	Q5IA38_AMBTC	Q5ia38 amborella t
570	83	6.0	787	2	Q3J591_RHOS4	Q3j591 rhodobacter	643	82	5.9	415	2	Q3K5U4_PSEPF	Q3k5u4 pseudomonas
571	83	6.0	802	2	Q8S278_DROME	Q8s278 drosophila	644	82	5.9	441	2	Q3VTV3_PROAE	Q3vtv3 prothecoch
572	83	6.0	1139	2	Q66DQ6_YERPS	Q66dq6 yersinia ps	645	82	5.9	446	1	CITN_KLEPN	P31602 klebsiella
573	83	6.0	1635	2	Q9C1I7_MYCGR	Q9c1i7 mycosphaere	646	82	5.9	459	2	Q70XF0_DROAU	Q70xf0 dromiclops
574	83	6.0	2159	2	Q8RUQ1_MAIZE	Q8ruq1 zea mays (m	647	82	5.9	465	2	Q74M77_NANEQ	Q74m77 nanoarchaeu
575	83	6.0	2159	2	Q8RVL1_MAIZE	Q8rvl1 zea mays (m	648	82	5.9	485	2	Q3RUF1_RALME	Q3ruf1 ralatonia m
576	82.5	5.9	265	2	Q3PG55_9GAMM	Q3pg55 shewanella	649	82	5.9	488	2	Q93YP9_ARATH	Q93yp9 arabidopsis
577	82.5	5.9	271	2	Q3ORV7_THIDN	Q3orv7 thiomicrosp	650	82	5.9	494	2	Q6F0R2_MESFL	Q6f0r2 mesoplasma
578	82.5	5.9	281	2	Q83BV7_COXBU	Q83bv7 coxiella bu	651	82	5.9	497	2	Q97A43_THEVO	Q97a43 thermoplas
579	82.5	5.9	337	2	Q59QT6_CANAL	Q59qt6 candida alb	652	82	5.9	497	2	Q421K2_DESHA	Q421k2 desulfitoba
580	82.5	5.9	346	2	Q8TQ84_METAC	Q8tq84 methanosarc	653	82	5.9	498	2	Q73GW3_WOLPM	Q73gw3 wolbachia p
581	82.5	5.9	361	2	Q31162_THICR	Q31162 thiomicrosp	654	82	5.9	514	2	Q44WQ6_9BURK	Q44wq6 burkholderi
582	82.5	5.9	368	2	Q72KY8_THET2	Q72ky8 thermus the	655	82	5.9	514	2	Q41NM2_9BURK	Q41nm2 burkholderi
583	82.5	5.9	391	1	EPF11_YEAST	P22140 saccharomyc	656	82	5.9	528	2	Q40LE0_DSAC	Q40le0 desulfuromo
584	82.5	5.9	400	2	Q7M916_WOLSU	Q7m916 wolinnella s	657	82	5.9	545	2	Q8FNV5_COREF	Q8fnv5 corynebacte
585	82.5	5.9	402	2	Q4HY99_GIBEZE	Q4hy99 gibberella	658	82	5.9	548	2	Q9A8F3_CAUCR	Q9a8f3 caulobacter
586	82.5	5.9	418	2	Q9HXM9_PSEAE	Q9hxm9 pseudomonas	659	82	5.9	557	1	YQ04_SCHPO	Q74537 schizosacch
587	82.5	5.9	432	2	Q35G00_9BRAD	Q35g00 bradyrhizob	660	82	5.9	557	2	Q8G3S6_BIFLO	Q8g3s6 bifidobacte
588	82.5	5.9	432	2	Q5PE07_SALPA	Q5pe07 salmonella	661	82	5.9	573	2	Q09932_CABEL	Q09932 caenorhabdi
589	82.5	5.9	437	2	Q81KE3_PLAF7	Q8ike3 plasmodium	662	82	5.9	594	2	Q7T709_9CLOS	Q7t709 citrus tris
590	82.5	5.9	439	2	Q4UYJ1_XANC8	Q4uyj1 xanthomonas	663	82	5.9	604	2	Q32UR9_SWICR	Q32ur9 smanthopsis
591	82.5	5.9	439	2	Q8P514_XANCP	Q8p514 xanthomonas	664	82	5.9	673	2	Q2RGF9_WOOTH	Q2rgf9 moorella th
592	82.5	5.9	441	2	Q3BPG6_XANC5	Q3bp66 xanthomonas	665	82	5.9	706	2	Q45283_CABEL	Q45283 caenorhabdi
593	82.5	5.9	443	2	Q2P6S4_XANOR	Q2p6s4 xanthomonas	666	82	5.9	727	2	Q5A438_CANAL	Q5a438 candida alb
594	82.5	5.9	448	2	Q6DVM4_9CRUS	Q6dvm4 triops long	667	82	5.9	748	2	Q6A6C2_PROAC	Q6a6c2 propionibac
595	82.5	5.9	451	2	Q82C18_STRAM	Q82ci8 streptomyce	668	82	5.9	766	2	Q3PHL5_PARDE	Q3phl5 paracoccus
596	82.5	5.9	452	2	Q9ZKR4_HELPJ	Q9zkr4 helicobacte	669	82	5.9	786	2	Q385S3_9TRYP	Q385s3 trypanosoma
597	82.5	5.9	453	2	Q5RCN8_PONPY	Q5rcn8 pongo pygma	670	82	5.9	801	2	Q3BYI7_XANC5	Q3byi7 xanthomonas
598	82.5	5.9	456	2	Q3K677_PSEPF	Q3k677 pseudomonas	671	82	5.9	807	2	Q6F8D1_ACIAD	Q6f8d1 acinetobact
599	82.5	5.9	462	2	Q6F0L1_MESFL	Q6f0l1 mesoplasma	672	82	5.9	884	2	Q8ER30_OCEIH	Q8er30 oceanobacil
600	82.5	5.9	471	2	Q8ASS9_LACPL	Q8ass9 lactocacill	673	82	5.9	893	2	Q51120_ENTHI	Q51120 entamoeba h
601	82.5	5.9	478	2	Q368A8_9GAMM	Q368a8 shewanella	674	82	5.9	1029	2	Q6KAN9_MOUSE	Q6kan9 mus musculu
602	82.5	5.9	478	2	Q2Z3J4_9GAMM	Q2z3j4 shewanella	675	82	5.9	1117	2	Q2UGL8_ASPOR	Q2ugl8 aspergillus
603	82.5	5.9	478	2	Q8EEL5_SHEON	Q8eel5 shewanella	676	82	5.9	1139	2	Q8ZC91_YERPE	Q8zc91 yersinia pe
604	82.5	5.9	482	2	Q3JD04_NITOC	Q3jd04 nitrosococc	677	82	5.9	1156	2	Q74WP6_YERPE	Q74wp6 yersinia pe
605	82.5	5.9	484	2	Q44H18_CHRSL	Q44h18 chromohalob	678	82	5.9	1168	1	ADCY6_HUMAN	Q43306 homo sapien
606	82.5	5.9	486	2	Q82YJ7_ENTFA	Q82yj7 enterococcu	679	82	5.9	1611	2	Q2U3Y1_ASPOR	Q2u3y1 aspergillus
607	82.5	5.9	494	1	NUAM_TIRIU	Q36834 trichophyco	680	81.5	5.9	205	2	Q8CYE3_STRR6	Q8cye3 streptococc
608	82.5	5.9	508	2	Q950R5_SPIPN	Q950r5 spizellomyco	681	81.5	5.9	205	2	Q97FC0_STRPN	Q97fc0 streptococc
609	82.5	5.9	543	2	Q7Z5I7_HUMAN	Q7z5i7 homo sapien	682	81.5	5.9	257	2	Q39XJ4_GOMG	Q39xj4 geobacter m
610	82.5	5.9	548	2	Q6AAJ7_PROAC	Q6aa17 propionibac	683	81.5	5.9	268	2	Q7MKQ7_VIBVY	Q7mkq7 vibrio vuln
611	82.5	5.9	596	1	AGP2_YEAST	P38090 saccharomyc	684	81.5	5.9	268	2	Q8D9M9_VIBVU	Q8d9m9 vibrio vuln
612	82.5	5.9	620	2	Q7SSR8_NEUCR	Q7ssr8 neurospora	685	81.5	5.9	292	2	Q4JT26_CORJK	Q4jt26 corynebacte
613	82.5	5.9	623	2	Q98P35_RHILO	Q98p35 rhizobium l	686	81.5	5.9	292	2	Q92DGO_LISIN	Q92dgo listeria in
614	82.5	5.9	636	2	Q5KSS3_9ECHI	Q5kss3 luidia quin	687	81.5	5.9	307	1	UPPP2_CLOAB	Q97kfe clostridium
615	82.5	5.9	640	2	Q6MB47_PARUW	Q6mb47 parachlamyid	688	81.5	5.9	321	2	Q94VH0_VARGO	Q94vh0 varanus gou

689	81.5	5.9	325	2	Q973Q6 SULTO	Q973q6 sulfolobus	762	81	5.8	411	2	Q2LS96_9DEL	Q2ls96 syntrophus
690	81.5	5.9	351	2	Q9FZ95_ARATH	Q9fz95 arabidopsis	763	81	5.8	422	2	Q6ESP5_ORISA	Q6esp5 oryza sativ
691	81.5	5.9	390	2	Q5BDJ8_EMENI	Q5bdj8 aspergillus	764	81	5.8	422	2	Q8Y1K4_RALSO	Q8y1k4 ralstonia s
692	81.5	5.9	399	2	Q8NCC4_HUMAN	Q8ncj4 homo sapien	765	81	5.8	423	2	Q3ZXM4_DEHSC	Q3zxm4 dehalococco
693	81.5	5.9	410	2	Q3NG59_FRATT	Q3ng59 francisella	766	81	5.8	438	2	Q8X4U5_ECO5C	Q8x4u5 escherichia
694	81.5	5.9	422	2	Q3VVI4_PROAE	Q3vvi4 prosthecoch	767	81	5.8	446	2	Q3GMM8_9GAMM	Q3gmw8 psychrobact
695	81.5	5.9	423	2	Q229R5_9GAMM	Q229r5 shewanella	768	81	5.8	461	1	PUUP_ECOLI	P76037 escherichia
696	81.5	5.9	423	2	Q360D7_9GAMM	Q360d7 shewanella	769	81	5.8	461	2	Q31Z22_SHIBS	Q31zz2 shigella bo
697	81.5	5.9	423	2	Q3SEP5_9GAMM	Q3sep5 shewanella	770	81	5.8	471	2	Q4S3V1_TETNG	Q4s3v1 tetraodon n
698	81.5	5.9	425	2	Q88CV8_PSEPK	Q88cv8 pseudomonas	771	81	5.8	479	2	Q87155_VIBCH	Q87155 vibrio chol
699	81.5	5.9	435	2	Q4YAK0_PLABE	Q4yak0 plasmodium	772	81	5.8	479	2	Q5H778_ECOLI	Q5h778 escherichia
700	81.5	5.9	436	2	Q7YZ03_CRYPTV	Q7yz03 cryptospori	773	81	5.8	485	2	Q6Z4N5_CAEBR	Q6z4n5 caenorhabdi
701	81.5	5.9	438	2	Q9HJD9_PSEAE	Q9hud9 pseudomonas	774	81	5.8	485	2	Q7PQT4_ANOGA	Q7pqt4 anopheles g
702	81.5	5.9	446	2	Q6OWD5_CAEBR	Q6owd5 caenorhabdi	775	81	5.8	487	2	Q9FRL3_ARATH	Q9frl3 arabidopsis
703	81.5	5.9	454	2	Q48KP6_PSE14	Q48kp6 pseudomonas	776	81	5.8	515	2	Q8TF71_HUMAN	Q8tf71 homo sapien
704	81.5	5.9	454	2	Q4ZVE0_PSEU2	Q4zve0 pseudomonas	777	81	5.8	531	2	Q3KCC6_PSEPF	Q3kcc6 pseudomonas
705	81.5	5.9	454	2	Q884R2_PSESM	Q884r2 pseudomonas	778	81	5.8	544	1	YRT3_CABEL	Q10046 caenorhabdi
706	81.5	5.9	454	2	Q89WU1_BRAJA	Q89wu1 bradyrhizob	779	81	5.8	548	2	Q8AAZ9_BACTN	Q8aa29 bacteroides
707	81.5	5.9	463	2	Q5DBJ2_SCHJA	Q5dbj2 schistosoma	780	81	5.8	550	2	Q7NZQ0_CHRVO	Q7nzq0 chromobacte
708	81.5	5.9	466	2	Q2OI38_9NEOP	Q2oi38 adoxophyes	781	81	5.8	578	2	Q47F72_DECAR	Q47f72 dechloromon
709	81.5	5.9	467	2	Q9W1Z2_DROME	Q9w1z2 drosophila	782	81	5.8	595	2	Q91MJ8_9PARA	Q91mj8 menangle vi
710	81.5	5.9	475	2	Q33RV8_9GAMM	Q33rv8 shewanella	783	81	5.8	603	2	Q3N807_9PROT	Q3n807 nitrosomona
711	81.5	5.9	482	2	Q3JEF5_NITOC	Q3jef5 nitrococcc	784	81	5.8	608	2	Q7QP79_GIALA	Q7qp79 giardia lam
712	81.5	5.9	485	2	O18063_CABEL	O18063 caenorhabdi	785	81	5.8	647	2	Q9GEU0_SAMVA	Q9geu0 samolus val
713	81.5	5.9	485	2	Q8SYB7_DROME	Q8syb7 drosophila	786	81	5.8	657	2	Q6XJ11_9ERIC	Q6xj11 sideroxylon
714	81.5	5.9	485	2	Q9W1Z3_DROME	Q9w1z3 drosophila	787	81	5.8	686	2	Q47L56_THEFY	Q47l56 thermobifid
715	81.5	5.9	487	2	Q2NA79_9SPHN	Q2na79 erythrobaet	788	81	5.8	710	2	O19824_9LAMI	O19824 cobananthus
716	81.5	5.9	510	2	Q34523_FASHE	Q34523 fasciola he	789	81	5.8	724	2	Q9GF06_9ERIC	Q9gf06 bonellia um
717	81.5	5.9	513	2	Q31ET8_THICR	Q31et8 thiomicrosp	790	81	5.8	734	2	Q9THV8_9GENT	Q9thv8 ronderletia
718	81.5	5.9	517	2	Q4HUN6_GIBZE	Q4hun6 gibberella	791	81	5.8	743	2	Q61LV8_CAEBR	Q61lv8 caenorhabdi
719	81.5	5.9	524	2	Q4SNU4_TETNG	Q4snu4 tetraodon n	792	81	5.8	829	2	Q3N9X2_9PROT	Q3n9x2 nitrosomona
720	81.5	5.9	527	2	Q2NHK7_9EURY	Q2nhk7 methanospa	793	81	5.8	865	2	Q2Y411_9ARCH	Q2y411 uncultured
721	81.5	5.9	535	2	Q3J012_RHOSA	Q3j012 rhodobacter	794	81	5.8	875	2	Q9V8U1_DROME	Q9v8u1 drosophila
722	81.5	5.9	535	2	O53111_RHOSH	O53111 rhodobacter	795	81	5.8	889	2	Q4V5E4_DROME	Q4v5e4 drosophila
723	81.5	5.9	570	2	Q2SVK8_BURTH	Q2svk8 burkholderi	796	81	5.8	971	2	Q68XX4_RCTY	Q68xx4 rickettsia
724	81.5	5.9	577	2	Q2U0M4_ASPOR	Q2u0m4 aspergillus	797	81	5.8	1102	2	Q88CW3_PSEPK	Q88cw3 pseudomonas
725	81.5	5.9	615	2	Q2U0X1_ASPOR	Q2u0x1 aspergillus	798	81	5.8	1150	2	Q2XJ80_PSEPU	Q2xj80 pseudomonas
726	81.5	5.9	618	2	O5AY73_EMENI	O5ay73 aspergillus	799	81	5.8	1207	2	Q4P6A9_USTMA	Q4p6a9 ustilago ma
727	81.5	5.9	623	2	O519X5_ENTHI	O519x5 entamoeba h	800	81	5.8	2186	1	POLG_CXB20	Q9ylg5 c genome po
728	81.5	5.9	626	2	O8XUM7_RALSO	O8xum7 ralstonia s	801	80.5	5.8	162	2	O7NNI6_GLOVI	Q7nni6 gloeobacter
729	81.5	5.9	711	2	Q6LH73_PHOPR	Q6lh73 photobacter	802	80.5	5.8	256	2	Q30UH8_THIDN	Q30uh8 thiomicrosp
730	81.5	5.9	713	2	Q9VWG4_DROME	Q9vwg4 drosophila	803	80.5	5.8	261	2	Q6LTB2_PHOPR	Q6ltb2 photobacter
731	81.5	5.9	724	2	Q8MRA8_DROME	Q8mra8 drosophila	804	80.5	5.8	288	2	O75JA0_GLOSI	Q75ja0 clonorchis
732	81.5	5.9	724	2	Q9TJZ6_9GENT	Q9tjz6 aleisis lugo	805	80.5	5.8	291	2	Q746X4_CROSL	Q746x4 geobacter s
733	81.5	5.9	731	2	Q9TJZ2_9GENT	Q9tjz2 hillia trif	806	80.5	5.8	296	2	Q3EEG9_ACTSC	Q3eeg9 actinobacil
734	81.5	5.9	732	2	Q9RTS0_9GENT	Q9rts0 pogonopus s	807	80.5	5.8	297	2	Q2VYV6_MAGSA	Q2vvyv6 magnetospir
735	81.5	5.9	734	2	Q98706_9GENT	Q98706 chlocoeca r	808	80.5	5.8	316	2	Q647F8_9VIRU	Q647f8 thermoprote
736	81.5	5.9	741	2	Q71QV9_9ASTR	Q71qv9 sigesbeckia	809	80.5	5.8	321	2	Q94VD4_9SAUR	Q94vd4 varanus pan
737	81.5	5.9	745	2	Q5UYP6_HALMA	Q5uyp6 haloarcula	810	80.5	5.8	324	2	Q83Z26_9GAMM	Q83z26 lamprocysti
738	81.5	5.9	855	2	Q6BGA9_PARTE	Q6bga9 paramecium	811	80.5	5.8	334	2	Q81HX6_PLAF7	Q81hx6 plasmodium
739	81.5	5.9	893	2	O54BC6_DICDI	O54bc6 dictyoateli	812	80.5	5.8	334	2	Q6AWL9_DROME	Q6awl9 drosophila
740	81.5	5.9	1402	2	Q610A1_CAEBR	Q610a1 caenorhabdi	813	80.5	5.8	334	2	Q81QJ7_DROME	Q81qj7 drosophila
741	81	5.8	226	2	Q4WVG5_BACCE	Q4wvg5 bacillus ce	814	80.5	5.8	354	1	PCBG_PROMT	Q46jw4 prochloroco
742	81	5.8	226	2	Q816R9_BACCR	Q816r9 bacillus ce	815	80.5	5.8	359	2	Q5HD36_STAAC	Q5hd36 staphylococ
743	81	5.8	228	2	Q41948_STAHH	Q41948 staphylococ	816	80.5	5.8	359	2	Q6G6F7_STAAS	Q6g6f7 staphylococ
744	81	5.8	273	2	Q3GLF0_9GAMM	Q3glf0 psychrobact	817	80.5	5.8	359	2	Q79ZZ9_STAAS	Q79zz9 staphylococ
745	81	5.8	287	2	Q5V2C4_HALMA	Q5v2c4 haloarcula	818	80.5	5.8	359	2	Q7A3I4_STAAN	Q7a3i4 staphylococ
746	81	5.8	293	1	Y417_CHLTR	Q84422 chlamydia t	819	80.5	5.8	359	2	Q99RB8_STAAM	Q99rb8 staphylococ
747	81	5.8	293	2	Q92WD8_RHIME	Q92wd8 rhizobium m	820	80.5	5.8	360	2	Q7Q2N8_ANOGA	Q7q2n8 anopheles g
748	81	5.8	296	2	Q3NMW5_THIDA	Q3nmw5 thioabacillu	821	80.5	5.8	366	2	Q8CWZ5_STRMU	Q8cwz5 streptococ
749	81	5.8	297	2	Q5NNK8_ZYMMO	Q5nnk8 zymomonas m	822	80.5	5.8	368	2	Q610H8_CAEBR	Q610h8 caenorhabdi
750	81	5.8	305	2	Q3W361_ANAVT	Q3w361 anabaena va	823	80.5	5.8	373	2	Q47GR9_DECAR	Q47gr9 dechloromon
751	81	5.8	305	2	Q5J3L3_RAT	Q5j3l3 rattus norv	824	80.5	5.8	378	2	Q5YN20_NOCFA	Q5yn20 nocardia fa
752	81	5.8	313	1	RBN_VIEVU	Q8dd62 vibrio vuln	825	80.5	5.8	393	2	Q8CMG2_STAEO	Q8cmg2 staphylococ
753	81	5.8	313	1	RBN_VIEVU	Q7mc07 vibrio vuln	826	80.5	5.8	393	2	O8NCN2_STAEB	Q8ncn2 staphylococ
754	81	5.8	315	2	Q3HAB6_TRJER	Q3hab6 trichodesmi	827	80.5	5.8	419	2	Q81NE5_BACAN	Q81ne5 bacillus an
755	81	5.8	347	2	Q2WPS2_CLOBE	Q2wps2 clostridium	828	80.5	5.8	433	2	Q74XD2_YERPE	Q74xd2 yersinia pe
756	81	5.8	369	2	Q3BU19_XANC5	Q3bu19 xanthomonas	829	80.5	5.8	433	2	Q66FD9_YERPS	Q66fd9 yersinia ps
757	81	5.8	375	1	PCBC_PROHO	P95507 prochloroth	830	80.5	5.8	438	2	Q8Z1Y7_YERPE	Q8z1y7 yersinia pe
758	81	5.8	375	2	Q5NPD7_ZYMMO	Q5npd7 zymomonas m	831	80.5	5.8	446	2	Q87VV4_PSESM	Q87vv4 pseudomonas
759	81	5.8	382	2	Q918P4_CYPCA	Q918p4 cyprinus ca	832	80.5	5.8	453	2	O51C11_TETTH	Q951c1 tetrahymena
760	81	5.8	396	2	Q83XE0_SHIFL	Q83xe0 shigella fl	833	80.5	5.8	453	2	Q618Q8_CAEBR	Q618q8 caenorhabdi
761	81	5.8	411	2	Q3NRE2_SHEFR	Q3nre2 shewanella	834	80.5	5.8	454	2	Q4K8P3_PSEF5	Q4k8p3 pseudomonas

835	80.5	5.8	465	2	Q48D16_PSE14	Q48D16 pseudomonas	908	80	5.7	451	2	Q6I7X8_LBPDU	Q6I7X8 leptotyrphlo
836	80.5	5.8	469	2	P93561_SOLTU	P93561 solanum tub	909	80	5.7	463	2	Q2V9L3_NITMU	Q2V9L3 nitrospir
837	80.5	5.8	470	2	Q9CP91_PASU	Q9CP91 pasteurella	910	80	5.7	472	2	Q9N5Q8_CAEEL	Q9N5Q8 caenorhabdi
838	80.5	5.8	472	2	Q44YB5_9BURK	Q44YB5 burkholderi	911	80	5.7	488	2	Q55GU7_DICDI	Q55GU7 dictyosteli
839	80.5	5.8	472	2	Q4LSU9_9BURK	Q4LSU9 burkholderi	912	80	5.7	488	2	Q966D7_CABEL	Q966D7 caenorhabdi
840	80.5	5.8	473	1	IOLT_BACSU	IOLT bacillus su	913	80	5.7	512	2	Q4WFT2_ASFFU	Q4WFT2 aspergillus
841	80.5	5.8	475	2	Q6LR41_PHOFR	Q6LR41 photobacter	914	80	5.7	516	2	Q4JUG1_ORYSA	Q4JUG1 oryza sativ
842	80.5	5.8	478	2	Q3QDD4_9GAMM	Q3QDD4 shewanella	915	80	5.7	528	2	Q5OZV7_ENTHA	Q5OZV7 entamoeba h
843	80.5	5.8	518	2	Q2SG80_9GAMM	Q2SG80 habella che	916	80	5.7	558	2	Q6XRA4_9BACT	Q6XRA4 uncultured
844	80.5	5.8	523	2	Q8RAX1_BACTN	Q8RAX1 bacteroides	917	80	5.7	657	2	Q6XJM6_9ERIC	Q6XJM6 inhabanell
845	80.5	5.8	528	2	Q5F6U6_NEIG1	Q5F6U6 neisseria g	918	80	5.7	671	2	Q7WXB7_RALEU	Q7WXB7 ralstonia e
846	80.5	5.8	528	2	Q7DDN3_NEIMB	Q7DDN3 neisseria m	919	80	5.7	686	2	Q3HT50_9BORA	Q3HT50 coidenia pr
847	80.5	5.8	528	2	Q9JRD7_NEIMA	Q9JRD7 neisseria m	920	80	5.7	699	2	Q8TLF3_9LAMI	Q8TLF3 hemiphragma
848	80.5	5.8	531	2	Q6KI84_MYCWO	Q6KI84 mycoplasma	921	80	5.7	702	2	Q19823_9LAMI	Q19823 alsobia sp.
849	80.5	5.8	534	2	Q2U2A8_ASFOR	Q2U2A8 aspergillus	922	80	5.7	714	2	Q73Y59_MYCPA	Q73Y59 mycobacteri
850	80.5	5.8	536	2	Q6MEN5_PARUM	Q6MEN5 parachlamyd	923	80	5.7	740	2	Q9TJUA_CSEOC	Q9TJUA cephalanthu
851	80.5	5.8	583	2	Q4ELG7_LISMO	Q4ELG7 listeria mo	924	80	5.7	740	2	Q8PG25_SALPA	Q8PG25 salmonella
852	80.5	5.8	590	1	CANI_YEAST	CANI yeast	925	80	5.7	740	2	Q8ZQN3_SALTY	Q8ZQN3 salmonella
853	80.5	5.8	595	2	Q3J3B7_RHOS4	Q3J3B7 rhodospir	926	80	5.7	850	2	Q3M4P3_ANAVT	Q3M4P3 anabaena va
854	80.5	5.8	637	2	Q21277_RECAM	Q21277 reclinomona	927	80	5.7	862	2	Q3VGR9_9SPHN	Q3VGR9 spingopyxi
855	80.5	5.8	660	2	Q89IN8_CLOTE	Q89IN8 clostridium	928	80	5.7	902	2	Q9K9X9_BACHD	Q9K9X9 bacillus ha
856	80.5	5.8	671	2	Q3AG29_RHOPA	Q3AG29 rhodopseudo	929	80	5.7	1067	2	Q8EJ80_SHEON	Q8EJ80 shewanella
857	80.5	5.8	690	2	Q2IM16_9DELT	Q2IM16 anaeromyxob	930	80	5.7	1123	2	Q9LYR7_ARATH	Q9LYR7 arabidopsis
858	80.5	5.8	728	2	Q98702_9GENT	Q98702 luculia gra	931	80	5.7	1202	2	Q4WP24_ASFFU	Q4WP24 aspergillus
859	80.5	5.8	732	2	Q9TJY9_CALCA	Q9TJY9 calycophyll	932	80	5.7	1480	2	Q6CSL2_YARLI	Q6CSL2 yarrowia li
860	80.5	5.8	751	2	Q3SOG1_RALME	Q3SOG1 ralstonia m	933	79.5	5.7	225	2	Q347J9_RHOPA	Q347J9 rhodopseudo
861	80.5	5.8	812	2	Q55KN8_CRYNE	Q55KN8 cryptococcu	934	79.5	5.7	235	2	Q6JCS9_9HEMI	Q6JCS9 aleuroplatu
862	80.5	5.8	812	2	Q5KAT6_CRYNE	Q5KAT6 cryptococcu	935	79.5	5.7	235	2	Q57RE9_SALCH	Q57RE9 salmonella
863	80.5	5.8	834	1	SL9A3_HUMAN	SL9A3 homo sapien	936	79.5	5.7	254	2	Q2ZGUO_CALSA	Q2ZGUO caldicellul
864	80.5	5.8	834	2	Q3MIW3_HUMAN	Q3MIW3 homo sapien	937	79.5	5.7	260	2	Q3EIP1_ATSCC	Q3EIP1 actinobacil
865	80.5	5.8	1019	2	Q3HAM2_TRIER	Q3HAM2 trichodesmi	938	79.5	5.7	261	2	Q31GZ8_THICR	Q31GZ8 thiomicrosp
866	80	5.7	210	2	Q5VWM7_HUMAN	Q5VWM7 homo sapien	939	79.5	5.7	264	2	Q6ITH2_CERBA	Q6ITH2 cercaria ba
867	80	5.7	226	2	Q81KJ3_BACAN	Q81KJ3 bacillus an	940	79.5	5.7	264	2	Q6ITI1_CERBA	Q6ITI1 cercaria ba
868	80	5.7	266	2	Q9HKP7_PSEAE	Q9HKP7 pseudomonas	941	79.5	5.7	293	2	Q3BJM4_PARDE	Q3BJM4 paracoccu
869	80	5.7	268	2	Q76FP9_STYPL	Q76FP9 styela plic	942	79.5	5.7	293	2	Q66D49_YERPS	Q66D49 yersinia ps
870	80	5.7	270	2	Q5JEB1_PYRKO	Q5JEB1 pyrococcus	943	79.5	5.7	296	2	Q93KC0_ERWCH	Q93KC0 erwinia chr
871	80	5.7	273	2	Q4AWQ6_9BURK	Q4AWQ6 polaromonas	944	79.5	5.7	296	2	Q6D4I7_ERWCT	Q6D4I7 erwinia car
872	80	5.7	277	2	Q3EQN3_BACTI	Q3EQN3 bacillus th	945	79.5	5.7	298	2	Q7U561_SINPX	Q7U561 synecococ
873	80	5.7	277	2	Q818H6_BACCR	Q818H6 bacillus th	946	79.5	5.7	298	2	Q8R257_MOUSE	Q8R257 mus musculu
874	80	5.7	285	2	Q6VQJ4_ONYPE	Q6VQJ4 onion yello	947	79.5	5.7	308	2	Q6CTH9_KIULA	Q6CTH9 kluveromyc
875	80	5.7	286	2	Q4MMH9_BACCE	Q4MMH9 bacillus ce	948	79.5	5.7	308	2	Q6ACY4_LEIXX	Q6ACY4 leifsonia x
876	80	5.7	286	2	Q63CM0_BACCCZ	Q63CM0 bacillus ce	949	79.5	5.7	312	2	Q5AF82_CANAL	Q5AF82 candida alb
877	80	5.7	286	2	Q6HK25_BACHK	Q6HK25 bacillus th	950	79.5	5.7	317	2	Q8UDK3_RHOBA	Q8UDK3 rhodopirell
878	80	5.7	286	2	Q81RV2_BACAN	Q81RV2 bacillus an	951	79.5	5.7	323	2	Q8DUD9_STRMU	Q8DUD9 streptococ
879	80	5.7	289	2	Q5DVU0_MIMPU	Q5DVU0 mimosa pud	952	79.5	5.7	325	2	Q4NG89_9MICC	Q4NG89 arthrobacte
880	80	5.7	291	2	Q8UIQ9_AGRT5	Q8UIQ9 agrobacteri	953	79.5	5.7	329	2	Q4SJT4_TETNG	Q4SJT4 tetraodon n
881	80	5.7	293	2	Q3KLT6_CHLTA	Q3KLT6 chlamydia t	954	79.5	5.7	342	2	Q5KY68_GROKA	Q5KY68 geobacillus
882	80	5.7	296	2	Q4MPJ0_BACCE	Q4MPJ0 bacillus ce	955	79.5	5.7	370	2	Q35QS4_9BRAD	Q35QS4 bradyrhizob
883	80	5.7	299	2	Q6AL50_DESPS	Q6AL50 desulfotale	956	79.5	5.7	371	2	Q2USP9_ASFOR	Q2USP9 aspergillus
884	80	5.7	301	2	Q2RGF6_MOOTH	Q2RGF6 moorella th	957	79.5	5.7	384	2	Q88ZD3_LACPL	Q88ZD3 lactobacill
885	80	5.7	306	2	Q2K6L6_RHET	Q2K6L6 rhizobium e	958	79.5	5.7	386	2	Q2KAL6_RHET	Q2KAL6 rhizobium e
886	80	5.7	312	2	Q4AJP5_CHRSL	Q4AJP5 chromohalob	959	79.5	5.7	388	2	Q4OEB4_9RHOB	Q4OEB4 jannaeschia
887	80	5.7	322	2	Q9GEH0_9MRTT	Q9GEH0 memecylon b	960	79.5	5.7	398	2	Q7NVC7_CHRVO	Q7NVC7 chromobacte
888	80	5.7	339	2	Q84ET1_9PROC	Q84ET1 prochloroth	961	79.5	5.7	405	2	Q77085_CAEEL	Q77085 caenorhabdi
889	80	5.7	341	2	Q47IB7_DECAR	Q47IB7 dechlorom	962	79.5	5.7	434	2	Q5E758_VIBF1	Q5E758 vibrio fisc
890	80	5.7	357	2	Q3POV7_NITHA	Q3POV7 nitrobacter	963	79.5	5.7	443	2	Q95AK6_9ASTR	Q95AK6 dialypetalu
891	80	5.7	363	2	Q8K839_CLOGS	Q8K839 clostridium	964	79.5	5.7	445	2	Q5S937_SVNY3	Q5S937 synecocyst
892	80	5.7	364	2	Q2V635_NITMU	Q2V635 nitrospir	965	79.5	5.7	445	2	Q6HKB2_BACHK	Q6HKB2 bacillus th
893	80	5.7	364	2	Q51723_BACNO	Q51723 bacteroides	966	79.5	5.7	453	2	Q2JYF1_RHET	Q2JYF1 rhizobium e
894	80	5.7	370	2	Q4DUS8_TRYCR	Q4DUS8 trypanosoma	967	79.5	5.7	454	2	Q3K8Y3_PSEPF	Q3K8Y3 pseudomonas
895	80	5.7	380	2	Q4RMW9_TETNG	Q4RMW9 tetraodon n	968	79.5	5.7	461	2	Q83RL6_SHIFL	Q83RL6 shigella fl
896	80	5.7	381	2	Q3IIN3_PSEHT	Q3IIN3 pseudosalter	969	79.5	5.7	466	2	Q4WS19_ASFFU	Q4WS19 aspergillus
897	80	5.7	386	2	Q4MM07_BACCE	Q4MM07 bacillus ce	970	79.5	5.7	466	2	Q4KY10_CAPBU	Q4KY10 capsella bu
898	80	5.7	387	2	Q551J1_CRYNE	Q551J1 cryptococcu	971	79.5	5.7	479	2	Q32144_SHISS	Q32144 shigella so
899	80	5.7	390	2	Q3NLO4_SHEFR	Q3NLO4 shewanella	972	79.5	5.7	483	2	Q31J91_THICR	Q31J91 thiomicrocro
900	80	5.7	391	2	Q6LY81_METMP	Q6LY81 methanococ	973	79.5	5.7	485	2	Q73Y55_MYCPA	Q73Y55 mycobacteri
901	80	5.7	409	2	Q4KKI5_PSEF5	Q4KKI5 pseudomonas	974	79.5	5.7	492	2	Q5H3W7_XANOR	Q5H3W7 xanthomonas
902	80	5.7	429	1	ARSB_STAUF	ARSB stauf	975	79.5	5.7	499	2	Q9UYPI_PYRAB	Q9UYPI pyrococcus
903	80	5.7	429	2	Q9AC73_STAAN	Q9AC73 staphylococ	976	79.5	5.7	500	2	Q4N1S4_THEPA	Q4N1S4 theileria p
904	80	5.7	438	2	Q3FAD4_9BURK	Q3FAD4 burkholderi	977	79.5	5.7	505	2	Q91GK1_BACST	Q91GK1 bacillus at
905	80	5.7	439	2	Q8FGX4_XANAC	Q8FGX4 xanthomonas	978	79.5	5.7	515	2	Q2UCU8_ASFOR	Q2UCU8 aspergillus
906	80	5.7	445	2	Q6NFO1_CORDB	Q6NFO1 corynebacte	979	79.5	5.7	516	2	Q2IL18_9DELT	Q2IL18 anaeromyxob
907	80	5.7	450	2	Q4MZY0_THEPA	Q4MZY0 theileria p	980	79.5	5.7	517	2	Q6MY57_ASFFU	Q6MY57 aspergillus

981	79.5	5.7	527	2	Q440H4_SOLUS	Q440h4 solibacter	1054	79	5.7	377	2	Q9LXX8_ARATH	Q9lxx8 arabidopsis
982	79.5	5.7	535	2	Q4PKJ2_ORYSA	Q4pkj2 oryza sativ	1055	79	5.7	381	2	Q6FDD6_AC1AD	Q6fdd6 acinetobact
983	79.5	5.7	539	1	FIXN_AGR77	P980c5 agrobacteri	1056	79	5.7	386	2	Q7NCK9_GLOVI	Q7nck9 gloebobact
984	79.5	5.7	542	2	Q2YKC6_BRUA2	P280c6 bruceella ab	1057	79	5.7	389	2	Q5LY93_BACFN	Q5ly93 bacteroides
985	79.5	5.7	542	2	Q8FWF3_BRUSU	Q8fwf3 bruceella su	1058	79	5.7	389	2	Q64Q89_BACFN	Q64q89 bacteroides
986	79.5	5.7	542	2	Q8YBW8_BRUME	Q8ybw8 bruceella me	1059	79	5.7	390	2	Q9X158_THEMA	Q9x158 thermotoga
987	79.5	5.7	542	2	Q577Q8_BRUAB	Q577q8 bruceella ab	1060	79	5.7	395	1	HMEB_ARCFU	Q29750 archaeoglob
988	79.5	5.7	544	2	Q64940_9CORA	Q64940 infectious	1061	79	5.7	400	2	Q3XTS0_9PROT	Q3xts0 magnetococc
989	79.5	5.7	559	2	Q5L073_GEOKA	Q5l073 geobacillus	1062	79	5.7	405	2	Q2RNM4_RHORU	Q2rnm4 rhodospiril
990	79.5	5.7	563	2	Q2U9X1_ASPOR	Q2u9x1 aspergillus	1063	79	5.7	409	2	Q4IANG_GIBZE	Q4ians gibberella
991	79.5	5.7	566	2	Q5BGM2_EMENI	Q5bgw2 aspergillus	1064	79	5.7	409	2	Q6E830_9HEMI	Q6e830 potnia glad
992	79.5	5.7	566	2	Q5BGM2_9HYME	Q5bnw2 aspergillus	1065	79	5.7	410	1	Y588_BUCAI	P57648 buchnera ap
993	79.5	5.7	570	2	Q8UQF7_AGR75	Q8uqf7 perga conde	1066	79	5.7	414	2	Q66R30_YEAST	Q66r30 saccharomyc
994	79.5	5.7	573	2	Q63FV4_BACCZ	Q6uf62 agrobacteri	1067	79	5.7	420	2	Q2RZ27_9SPHI	Q2rzz7 salinibacte
995	79.5	5.7	573	2	Q81V13_BACAN	Q63fv4 bacillus ce	1068	79	5.7	423	2	Q3Q6K6_9GAMM	Q3q6k6 shewanella
996	79.5	5.7	588	2	Q41543_GIBBEZ	Q81v13 bacillus an	1069	79	5.7	429	2	Q83Y88_BURPS	Q83yg8 burkholderi
997	79.5	5.7	593	2	Q6BM61_DESHA	Q41543 gibberella	1070	79	5.7	438	2	Q7ACT1_ECO57	Q7act1 escherichia
998	79.5	5.7	596	2	Q5Z6S8_ORYSA	Q6bm61 debaryomyce	1071	79	5.7	438	2	Q8FGD5_ECOL6	Q8fgd5 escherichia
999	79.5	5.7	598	2	Q7CZ11_AGR75	Q5z6s8 oryza sativ	1072	79	5.7	439	2	Q4WKR6_ASPFU	Q4wkr6 aspergillus
1000	79.5	5.7	600	2	Q6LKC0_PHOPR	Q7cz11 agrobacteri	1073	79	5.7	442	2	Q4W667_VIBCH	Q4w667 vibrio chol
1001	79.5	5.7	603	2	Q33H54_METHU	Q6lkc0 photobacter	1074	79	5.7	443	2	Q6LKM2_PHOPR	Q6lkm2 photobacter
1002	79.5	5.7	613	2	Q8CBQ1_MOUSE	Q33h54 methanospir	1075	79	5.7	444	2	Q7VT98_BORPE	Q7vt98 bordetella
1003	79.5	5.7	628	2	Q67ML1_SYMTH	Q8cbq1 mus musculu	1076	79	5.7	444	2	Q7W2C1_BORPA	Q7w2c1 bordetella
1004	79.5	5.7	632	2	Q9AZ47_BPSP6	Q67ml1 symbiobacte	1077	79	5.7	444	2	Q7WR89_BORBR	Q7wr89 bordetella
1005	79.5	5.7	635	2	Q2RAP8_ORYSA	Q9az47 enterobacte	1078	79	5.7	444	2	Q9KKW1_VIBCH	Q9kkw1 vibrio chol
1006	79.5	5.7	639	2	Q5WC83_BACSK	Q2rap8 oryza sativ	1079	79	5.7	446	2	Q6L0U0_PICTO	Q6l0u0 picrophilus
1007	79.5	5.7	643	2	Q2RU29_RHORU	Q5wc83 bacillus cl	1080	79	5.7	447	2	Q6GER0_STAAR	Q6ger0 staphylococ
1008	79.5	5.7	669	2	Q6USQ3_9DIPS	Q2ru29 rhodospiril	1081	79	5.7	453	2	Q8Y8B8_LISMO	Q8y8b8 listeria mo
1009	79.5	5.7	677	2	Q6CY48_KLULA	Q6usq3 valeriana e	1082	79	5.7	456	2	Q9H1D5_9HEAC	Q9hid5 thermoplas
1010	79.5	5.7	695	2	Q9TJS9_9GENT	Q6cy48 kluyveromyc	1083	79	5.7	456	2	Q7PB27_RICSI	Q7pb27 rickettsia
1011	79.5	5.7	697	1	HAK4_ORYSA	Q9tjs9 mussaenda a	1084	79	5.7	457	2	Q4N1S2_9HEPA	Q4n1s2 theileria p
1012	79.5	5.7	699	2	Q91VL7_MOUSE	Q6ysa9 oryza sativ	1085	79	5.7	459	2	Q3BEP6_9FALC	Q3bep6 spizaetua n
1013	79.5	5.7	726	2	Q2ZK71_CALSA	Q91vl7 mus musculu	1086	79	5.7	464	2	Q8RC72_THETN	Q8rc72 thermoanaer
1014	79.5	5.7	733	2	Q44XZ0_CHRSL	Q2zk71 caldicellul	1087	79	5.7	465	2	Q440N7_SOLUS	Q440n7 solibacter
1015	79.5	5.7	734	2	Q4RWS7_TETNG	Q44xz0 chromohalob	1088	79	5.7	468	2	Q2QWH8_ORYSA	Q2qwh8 oryza sativ
1016	79.5	5.7	735	2	Q4DAB4_TRYCR	Q4rws7 tetraodon n	1089	79	5.7	473	2	Q16252_CABEL	Q16252 caenorhabd
1017	79.5	5.7	741	2	Q32132_9ASTR	Q4dab4 trypanosoma	1090	79	5.7	477	2	Q3NWM8_9GAMM	Q3nwm8 gamma
1018	79.5	5.7	831	1	SL9A3_RAT	Q32132 chrysanthem	1091	79	5.7	479	2	O16926_CABEL	O16926 caenorhabd
1019	79.5	5.7	878	2	Q8MKL0_DROME	P26433 rattus norv	1092	79	5.7	481	2	Q62EY5_BURMA	Q62ey5 burkholderi
1020	79.5	5.7	890	2	Q2Y5X4_NITMU	Q8mk10 drosophila	1093	79	5.7	489	2	Q97E89_CIOAB	Q97ee9 clostridium
1021	79.5	5.7	976	2	Q56VU4_BLOGR	Q2y5x4 nitrosospir	1094	79	5.7	491	2	Q4KH41_PSEF5	Q4kh41 pseudomona
1022	79.5	5.7	1078	2	Q55F45_DICDI	Q56vu4 blumeria gr	1095	79	5.7	492	2	Q5A405_CANAL	Q5a405 candida alb
1023	79.5	5.7	1163	2	Q2U2G2_ASPOR	O55f45 dictyosteli	1096	79	5.7	497	2	Q7TNN9_RAT	Q7tnn9 rattus norv
1024	79.5	5.7	1321	2	Q4RSL1_TETNG	Q2u2g2 aspergillus	1097	79	5.7	498	2	Q4X148_ASPFU	Q4x148 aspergillus
1025	79.5	5.7	1529	2	Q5HB09_EHRRW	Q4rs11 tetraodon n	1098	79	5.7	501	2	Q5TMB6_CHICK	Q5tmb6 gallus gall
1026	79.5	5.7	1539	2	Q4UE92_9THAN	Q5hb09 ehrlichia r	1099	79	5.7	517	2	Q9XYS3_DICDI	Q9xys3 dictyosteli
1027	79.5	5.7	1569	2	Q5FEL3_EHRRW	Q4ue92 theileria a	1100	79	5.7	518	2	Q3CGR2_9HEET	Q3cgr2 thermoanaer
1028	79.5	5.7	1591	2	Q5FFL1_EHRRG	O5f11 ehrlichia r	1101	79	5.7	524	2	Q4W158_ASPFU	Q4wi58 aspergillus
1029	79.5	5.7	1591	2	Q42211_NECWA	Q5ffl1 necturus ma	1102	79	5.7	526	2	Q4J830_SULAC	Q4j830 sulfolobus
1030	79.5	5.7	172	1	NU6M_PETMA	Q42211 necturus ma	1103	79	5.7	534	2	Q88Z37_LACPL	Q88z37 lactobacill
1031	79.5	5.7	183	2	Y507_HAEIN	Q35544 petromyzon	1104	79	5.7	534	2	Q88Z37_9BRAD	Q88z37 bradyrhizob
1032	79.5	5.7	183	2	Q4QN39_HAEI8	P44010 haemophilus	1105	79	5.7	551	2	Q421G2_DESHA	Q421g2 desulfitoba
1033	79.5	5.7	192	2	Q6CYK5_ERWCT	Q4qn39 haemophilus	1106	79	5.7	585	2	Q60UUI_CAEBR	Q60uu1 caenorhabd
1034	79.5	5.7	226	2	Q6HCD0_BACHK	Q6cyk5 erwinia car	1107	79	5.7	595	2	Q837Q4_ENTFA	Q837q4 enterococc
1035	79.5	5.7	229	2	Q8XIK9_CLOPE	Q6hcd0 bacillus th	1108	79	5.7	602	2	Q70X18_9META	Q70x18 rhyncholest
1036	79.5	5.7	248	2	Q50BH3_LACRE	Q8xik9 clostridium	1109	79	5.7	657	2	Q3SUK6_NITWN	Q3suk6 nitrobacter
1037	79.5	5.7	269	2	Q3QSB7_9RHOB	O50eh3 lactobacill	1110	79	5.7	658	2	Q6XJL0_9ERIC	Q6xjl0 nesoluma po
1038	79.5	5.7	282	2	Q5K125_9ROSI	Q3qsb7 silicibacte	1111	79	5.7	658	2	Q6XJL0_9ERIC	Q6xjl0 nesoluma po
1039	79.5	5.7	282	2	Q4ULV8_RICPE	O5k125 populus tre	1112	79	5.7	669	1	NU5M_AEATH	Q6xjl0 nesoluma po
1040	79.5	5.7	289	2	Q946J9_MEDTR	Q4ulv8 rickettsia	1113	79	5.7	682	2	Q69UI4_ORYSA	Q69ui4 oryza sativ
1041	79.5	5.7	289	2	Q5U7L0_9FABA	Q946j9 medicago tr	1114	79	5.7	685	2	O19822_9LAMI	O19822 alsobia sp.
1042	79.5	5.7	293	1	Y543_CHLPN	Q5u7l0 glycyrrhiza	1115	79	5.7	687	2	Q3HT37_9BORA	Q3ht37 tiquilia hi
1043	79.5	5.7	293	2	Q9KDZ5_BACHD	Q9kdz5 chlamydia p	1116	79	5.7	687	2	Q3HT37_9BORA	Q3ht37 tiquilia hi
1044	79.5	5.7	300	2	Q6HM61_BACHK	Q9kdz5 bacillus ha	1117	79	5.7	688	2	Q3HT35_9BORA	Q3ht35 tiquilia hi
1045	79.5	5.7	307	2	Q9UTQ9_NEIMA	Q6hm61 bacillus th	1118	79	5.7	688	2	Q8M8X1_9ASTE	Q8m8x1 sphenoclea
1046	79.5	5.7	310	2	Q7MQN1_VIBVY	Q9jtc9 neisseria m	1119	79	5.7	723	2	Q9TIW2_9ASTE	Q9tiw2 phacelia ca
1047	79.5	5.7	310	2	Q8DAH5_VIBVU	Q7mqn1 vibrio vuln	1120	79	5.7	733	2	Q3S193_MOUSE	Q3s193 mus musculu
1048	79.5	5.7	322	2	O5PIY1_AZOSE	Q8dah5 vibrio vuln	1121	79	5.7	738	2	Q9TJUS_MORCI	Q9tj88 morinda cic
1049	79.5	5.7	341	2	Q2QWH7_ORYSA	O5piy1 azoarcus sp	1122	79	5.7	746	2	Q40TLB7_DIGAP	Q40tlb7 digitalis p
1050	79.5	5.7	354	2	Q97CL9_9THEVO	Q2qwh7 oryza sativ	1123	79	5.7	758	2	Q9OR23_DESAC	Q9or23 desulfuromo
1051	79.5	5.7	369	2	Q8PL40_XANAC	Q97cl9 thermoplas	1124	79	5.7	819	2	O31582_BACSU	O31582 bacillus su
1052	79.5	5.7	372	2	Q6G1A8_STAAR	Q8pl40 xanthomonas	1125	79	5.7	830	2	Q2V621_CANAL	Q2v621 candida alb
1053	79.5	5.7	373	2	Q8LBH3_ARATH	Q6gia8 staphylococ	1126	79	5.7	1046	2	Q2X4H3_9GAMM	Q2x4h3 shewanella

Q8lbh3 arabidopsis

1127	79	5.7	1067	2	Q3QB9Y_9GAMM	Q3q9y9 shewanella	1200	78.5	5.6	474	2	Q4QK73 HAB18	Q4qk73 haemophilus
1128	79	5.7	1068	2	Q2ZNP8_SHEPU	Q2znp8 shewanella	1201	78.5	5.6	475	2	Q49VD6_STASI	Q49vd6 staphylococ
1129	79	5.7	1166	2	Q44EW7_CHRSL	Q44ew7 chromohalob	1202	78.5	5.6	478	2	Q5AY52_EMENI	Q5ay52 aspergillus
1130	79	5.7	1501	2	Q8CIQ9_MOUSE	Q8ciq9 mus musculus	1203	78.5	5.6	479	2	Q5GCA8_RHOGE	Q5gca8 rhodocyclus
1131	79	5.7	1501	2	Q3TDN0_MOUSE	Q3tdn0 mus musculus	1204	78.5	5.6	482	2	Q83AQ0_COXBU	Q83aq0 coxiella bu
1132	79	5.7	1521	2	Q3UUL8_MOUSE	Q3uul8 mus musculus	1205	78.5	5.6	482	2	Q85MF7_9NEOP	Q85mf7 cyrestia th
1133	79	5.7	1521	2	Q8QZ28_MOUSE	Q8qz28 mus musculus	1206	78.5	5.6	483	2	Q2LB19_9NEOP	Q2lb19 thauria ali
1134	79	5.7	1521	2	Q8CGS3_MOUSE	Q8cgs3 mus musculus	1207	78.5	5.6	487	2	Q3ZEF8_EPIFL	Q3zef8 epidermophy
1135	79	5.7	1521	2	Q8CIP6_MOUSE	Q8cip6 mus musculus	1208	78.5	5.6	493	2	Q9VOT0_PVRAB	Q9vot0 pyrococcus
1136	79	5.7	1709	2	Q6LIW5_CABER	Q6liw5 caenorhabdi	1209	78.5	5.6	501	2	Q8FB10_ESCHICH	Q8fb10 escherichia
1137	79	5.7	1794	2	Q4QGV5_LEIMA	Q4qgv5 leishmania	1210	78.5	5.6	502	2	Q3GYP4_9ACTO	Q3gyp4 nocardioide
1138	79	5.7	2198	2	Q18990_CABEL	Q18990 caenorhabdi	1211	78.5	5.6	505	2	Q3ICQ3_PSEHT	Q3icq3 pseudocalt
1139	78.5	5.6	169	2	Q9HSA7_HALSA	Q9hsa7 halobacteri	1212	78.5	5.6	510	2	Q9B8Y2_FASHE	Q9b8y2 fasciola he
1140	78.5	5.6	182	2	Q3CSW3_ALTAT	Q3csw3 pseudocalt	1213	78.5	5.6	512	2	Q6ZMD2_HUMAN	Q6zmd2 homo sapien
1141	78.5	5.6	188	2	Q493Y2_BLOPB	Q493y2 blochmannia	1214	78.5	5.6	518	2	Q3VHK6_SHINGOPY	Q3vhk6 shingopyxi
1142	78.5	5.6	241	1	MCBE_ECOLI	P05528 escherichia	1215	78.5	5.6	526	2	Q6MUB7_MYCMS	Q6mub7 mycoplasma
1143	78.5	5.6	242	2	Q6LFC6_PHOPR	Q6lfc6 photobacter	1216	78.5	5.6	536	2	Q2U3S4_ASPOR	Q2u3s4 aspergillus
1144	78.5	5.6	247	2	Q3BR73_BRARE	Q3br73 brachydanio	1217	78.5	5.6	554	2	Q2W3Z5_MAGSA	Q2w3z5 magnetospir
1145	78.5	5.6	254	2	Q4SVF4_TETNG	Q4svf4 tetraodon n	1218	78.5	5.6	559	2	Q6DCE3_XENLA	Q6dce3 xenopus lae
1146	78.5	5.6	259	2	Q3CMD0_ALTAT	Q3cmd0 pseudocalt	1219	78.5	5.6	574	2	Q3SON5_RALME	Q3son5 ralstonia m
1147	78.5	5.6	264	2	Q6ITH4_CERBA	Q6ith4 cercaria ba	1220	78.5	5.6	579	2	Q5O465_MYCTU	Q5o465 mycobacteri
1148	78.5	5.6	264	2	Q6ITI2_CERBA	Q6iti2 cercaria ba	1221	78.5	5.6	580	2	Q4MPJ8_BACCE	Q4mpj8 bacillus ce
1149	78.5	5.6	281	2	Q5J371_PYRKO	Q5j371 pyrococcus	1222	78.5	5.6	583	2	Q95OT2_HVACU	Q95ot2 hyaloraphid
1150	78.5	5.6	293	2	Q4WBE1_9ACAR	Q4wbe1 leptotrombi	1223	78.5	5.6	591	2	Q8SXJ9_DROME	Q8sxj9 drosophila
1151	78.5	5.6	298	2	Q65V25_MANSM	Q65v25 mantheimia	1224	78.5	5.6	591	2	Q9V9U1_DROME	Q9v9u1 drosophila
1152	78.5	5.6	298	2	Q73T54_MYCPA	Q73t54 mycobacteri	1225	78.5	5.6	609	2	Q2Y4R6_9ARCH	Q2y4r6 uncultured
1153	78.5	5.6	302	2	Q4L8C2_STAHP	Q4l8c2 staphylococ	1226	78.5	5.6	620	2	Q2TK00_9ERIC	Q2tk00 pelletiera
1154	78.5	5.6	314	2	Q97OC7_SULTO	Q97oc7 sulfolobus	1227	78.5	5.6	622	1	COX1_BACSU	P24010 bacillus su
1155	78.5	5.6	316	2	Q7EY23_ORYSA	Q7ey23 oryza sativ	1228	78.5	5.6	624	2	Q9LYR6_ARATH	Q9lyr6 arabidopsis
1156	78.5	5.6	320	2	Q9BBU4_9MYRT	Q9bbu4 warneckea m	1229	78.5	5.6	634	2	Q3VQ16_9CHLB	Q3vq16 peridictyon
1157	78.5	5.6	320	2	Q7ZWS9_XENLA	Q7zws9 xenopus lae	1230	78.5	5.6	641	2	Q5NM95_ZYMOA	Q5nm95 zymomonas m
1158	78.5	5.6	321	2	Q9BBV9_9MYRT	Q9bbv9 mouriri hel	1231	78.5	5.6	652	2	Q9TIX1_9ASTE	Q9tix1 codon schen
1159	78.5	5.6	324	2	Q21VA0_RHOPA	Q21va0 rhodopseudo	1232	78.5	5.6	682	2	Q6USQ0_9DIPS	Q6usq0 valeriana c
1160	78.5	5.6	324	2	Q5F546_NEIG1	Q5f546 neisseria g	1233	78.5	5.6	686	2	Q3HT46_9BORA	Q3ht46 tiqullaia gr
1161	78.5	5.6	325	2	Q9MRZ1_9MYRT	Q9mrz1 heterocent	1234	78.5	5.6	691	2	Q9JYK5_BRANA	Q9jyk5 brassica na
1162	78.5	5.6	330	2	Q9VU64_DROME	Q9vu64 drosophila	1235	78.5	5.6	699	2	Q2LYT2_DROPHI	Q2lyt2 drosophila
1163	78.5	5.6	333	2	Q3DBR7_STRAG	Q3db7 streptococ	1236	78.5	5.6	732	2	Q98707_9GENT	Q98707 musaenda e
1164	78.5	5.6	333	2	Q3KOB7_STRAI	Q3kob7 streptococ	1237	78.5	5.6	732	2	Q9TJP6_9GENT	Q9tjp6 strumpfia m
1165	78.5	5.6	333	2	Q3KDR3_STRAG	Q3kdr3 streptococ	1238	78.5	5.6	734	2	Q9TJQ0_9GENT	Q9tjq0 rogiera suf
1166	78.5	5.6	340	2	Q8G845_BIFLO	Q8g845 bifidobacte	1239	78.5	5.6	744	2	Q32645_MENTR	Q32645 menyanthes
1167	78.5	5.6	356	2	Q8DRT2_STRMU	Q8drt2 streptococ	1240	78.5	5.6	779	2	Q6A6U5_PROAC	Q6a6u5 propionibac
1168	78.5	5.6	362	2	Q3RJB4_XYLFA	Q3rjb4 xyella fab	1241	78.5	5.6	798	2	Q2KGF8_MAGGR	Q2kgf8 magnaporthe
1169	78.5	5.6	366	1	Y1196_METJA	Q58596 methanococ	1242	78.5	5.6	803	2	Q3FZU0_9DELT	Q3fzu0 pelobacter
1170	78.5	5.6	384	2	Q3CNM8_ALTAT	Q3cnm8 pseudocalt	1243	78.5	5.6	825	2	Q6N215_RHOPA	Q6n215 rhodopseudo
1171	78.5	5.6	389	2	Q4ZWE3_PSEUM	Q4zwe3 pseudomonas	1244	78.5	5.6	829	2	Q46G21_METBA	Q46g21 methanosarc
1172	78.5	5.6	389	2	Q93TD9_PSEYM	Q93td9 pseudomonas	1245	78.5	5.6	863	2	Q92L62_RHIME	Q92l62 rhizobium m
1173	78.5	5.6	389	2	Q87WD8_PSESM	Q87wd8 pseudomonas	1246	78.5	5.6	864	2	Q4L5U5_STAHP	Q4l5u5 staphylococ
1174	78.5	5.6	393	2	Q639K7_BACCC	Q639k7 bacillus ce	1247	78.5	5.6	898	2	Q5I5C8_TRYCR	Q5i5c8 cyprinid ep
1175	78.5	5.6	395	2	Q612Y3_CABER	Q612y3 caenorhabdi	1248	78.5	5.6	930	2	Q4E2X6_TRYCR	Q4exx6 trypanosoma
1176	78.5	5.6	397	2	Q8KW37_9RHOB	Q8kw37 ruegeria sp	1249	78.5	5.6	1093	2	Q84W30_ARATH	Q84w30 arabidopsis
1177	78.5	5.6	397	2	Q5NHL1_FRAAT	Q5nhl1 francisella	1250	78.5	5.6	1289	2	Q7RKA2_PLAYO	Q7rka2 plasmodium
1178	78.5	5.6	405	2	Q9U2M5_CABEL	Q9u2m5 caenorhabdi	1251	78.5	5.6	1325	2	Q64533_ARATH	Q64533 arabidopsis
1179	78.5	5.6	411	2	Q2JXD1_9CYAN	Q2jxd1 cyanobacter	1252	78.5	5.6	1356	2	Q9QH56_9ALPH	Q9qh56 gallid herp
1180	78.5	5.6	411	2	Q89ZC7_BACTN	Q89zc7 bacteroides	1253	78.5	5.6	3172	2	Q4QAV5_LEIMA	Q4qav5 leishmania
1181	78.5	5.6	412	2	Q2MGY8_STAAN	Q2mgy8 staphylococ	1254	78.5	5.6	4856	2	Q7PZB3_ANOGA	Q7pzb3 anopheles g
1182	78.5	5.6	412	2	Q7A856_STAAN	Q7a856 staphylococ	1255	78.5	5.6	158	2	Q9XW23_CABEL	Q9xw23 caenorhabdi
1183	78.5	5.6	412	2	Q9X844_STAAM	Q9x844 staphylococ	1256	78.5	5.6	197	2	Q98CZ0_RHILO	Q98cz0 rhizobium l
1184	78.5	5.6	414	2	Q4CWZ9_TRYCR	Q4cwz9 trypanosoma	1257	78.5	5.6	205	2	Q5VWM8_HUMAN	Q5vwm8 homo sapien
1185	78.5	5.6	419	2	Q3PID7_9GAMM	Q3pid7 shewanella	1258	78.5	5.6	209	2	Q5ANB5_DICDI	Q5anb5 dictyosteli
1186	78.5	5.6	436	2	Q4K6F5_PSEF5	Q4k6f5 pseudomonas	1259	78.5	5.6	227	2	Q8HMJ0_9TELE	Q8hmj0 carapus ber
1187	78.5	5.6	437	2	Q3LIW2_THICR	Q3liw2 thiomicrosp	1260	78.5	5.6	231	2	Q5BLJ3_BRARE	Q5blj3 brachydanio
1188	78.5	5.6	438	2	Q48IS3_PSEL4	Q48is3 pseudomonas	1261	78.5	5.6	261	2	Q33X10_9GAMM	Q33x10 shewanella
1189	78.5	5.6	442	2	Q2L207_BORAR	Q2l207 bordetella	1262	78.5	5.6	262	2	Q98A38_RHILO	Q98a38 rhizobium l
1190	78.5	5.6	443	2	Q57JM1_SALCH	Q57jm1 salmonella	1263	78.5	5.6	263	2	Q2S8N7_9GAMM	Q2s8n7 habella che
1191	78.5	5.6	443	2	Q8ZLW4_SALTY	Q8zlw4 salmonella	1264	78.5	5.6	268	2	Q6LZZ9_METMP	Q6lzz9 methanococ
1192	78.5	5.6	447	2	Q6CTW0_ERMCT	Q6ctw0 erwinia car	1265	78.5	5.6	295	2	Q6F8F8_XENTR	Q6f8f8 xenopus tro
1193	78.5	5.6	457	2	Q410S4_KINRA	Q410s4 kinococcus	1266	78.5	5.6	299	2	Q9QX34_MOUSE	Q9qx34 mus musculu
1194	78.5	5.6	458	2	Q4HHT9_CAMCO	Q4hht9 campylobact	1267	78.5	5.6	307	2	Q9JYR8_NEIME	Q9jyr8 neisseria m
1195	78.5	5.6	464	2	Q979J8_THEVO	Q979j8 thetoplasm	1268	78.5	5.6	327	2	Q974Q0_SUITO	Q974q0 sulfolobus
1196	78.5	5.6	470	2	Q6C8J1_YARLI	Q6c8j1 varrowia li	1269	78.5	5.6	331	2	Q5JYAL_HUMAN	Q5jyal homo sapien
1197	78.5	5.6	470	2	Q31XW0_SYNPF	Q31xw0 synecococ	1270	78.5	5.6	335	1	MRAY_CHLMU	Q9plg6 chlamydia m
1198	78.5	5.6	470	2	Q5N109_SYNCP6	Q5n109 synecococ	1271	78.5	5.6	335	2	Q41WK3_DESHA	Q41wk3 desulfotoba
1199	78.5	5.6	471	2	Q6AB86_PROAC	Q6ab86 propionibac	1272	78.5	5.6	338	2	Q9KY69_STRCO	Q9ky69 streptomyce

1273	78	5.6	340	2	Q7S314	NEUCR	Q7a314	neurospora	1346	78	5.6	834	2	Q8E9A7	SHEON	Q8e9a7	shewanella
1274	78	5.6	353	2	Q800J7	METMA	Q8q0j7	methanosarc	1347	78	5.6	1087	2	Q2K223	RHET	Q2k223	rhizobium e
1275	78	5.6	358	2	Q3CEJ9	THEET	Q3cej9	thermoansar	1348	78	5.6	1533	2	Q4YU69	PLABE	Q4yu69	plasmodium e
1276	78	5.6	366	2	Q6SF48	BACLD	Q6sf48	bacillus li	1349	77.5	5.6	199	2	Q4QEX1	LEJMA	Q4qex1	leishmania
1277	78	5.6	379	2	Q8SL69	9TREM	Q8sl69	chimaerohem	1350	77.5	5.6	206	2	Q5KY19	GEOKA	Q5ky19	geobacillus
1278	78	5.6	382	2	Q92IS9	RICKET	Q92is9	rickettsia	1351	77.5	5.6	212	2	Q9KAJ4	BACHD	Q9kaj4	bacillus ha
1279	78	5.6	386	2	Q5P1K0	AZOSE	Q5p1k0	azoarcus sp	1352	77.5	5.6	229	1	YR809	MIMIV	YR809	mimivirus
1280	78	5.6	388	2	Q9RTZ5	DEIRA	Q9rtz5	deinococcus	1353	77.5	5.6	243	2	Q93RC4	ECOLI	Q93rc4	escherichia
1281	78	5.6	392	2	Q9ESM5	RAT	Q9esm5	rattus norv	1354	77.5	5.6	245	2	Q3HI18	TRIER	Q3hi18	trichodesmi
1282	78	5.6	396	2	Q5YMB7	SALCH	Q5ymb7	salmonella	1355	77.5	5.6	248	2	Q3VHY8	9CHLB	Q3vhy8	pelodictyon
1283	78	5.6	396	2	Q5PE30	SALPA	Q5pe30	salmonella	1356	77.5	5.6	256	2	Q3IDA4	PSEHT	Q3ida4	pseudoalter
1284	78	5.6	396	2	Q8ZNJ7	SALTY	Q8znj7	salmonella	1357	77.5	5.6	260	2	Q7VV38	BORPE	Q7vv38	bordetella
1285	78	5.6	396	2	Q8Z581	SALTI	Q8z581	salmonella	1358	77.5	5.6	260	2	Q7WU07	BORPE	Q7wu07	bordetella
1286	78	5.6	408	2	Q81RH3	BACAN	Q81rh3	bacillus an	1359	77.5	5.6	260	2	Q7WN67	BORBR	Q7wn67	bordetella
1287	78	5.6	408	1	KCNK3	MOUSE	Q35111	mus musculu	1360	77.5	5.6	268	2	Q8U2B7	PYRBR	Q8u2b7	pyrococcus
1288	78	5.6	409	2	Q6HZP9	BACAN	Q6hzp9	bacillus an	1361	77.5	5.6	276	2	Q4CXN5	TRYCR	Q4cxn5	trypanosoma
1289	78	5.6	409	2	Q6HUQ7	BACHK	Q6huq7	bacillus th	1362	77.5	5.6	283	2	Q92WH1	RHIME	Q92wh1	rhizobium m
1290	78	5.6	411	1	KCNK3	RAT	O54912	rattus norv	1363	77.5	5.6	287	2	Q6NJG1	CORDI	Q6njg1	corynebacte
1291	78	5.6	414	1	YMB7	YEAST	Q04835	saccharomyc	1364	77.5	5.6	288	2	Q9MF61	BETVU	Q9mf61	beta vulgar
1292	78	5.6	415	2	Q35X3	9GAMM	Q35xx3	shewanella	1365	77.5	5.6	288	2	Q9M4S9	ALLCE	Q9m4s9	allium cepa
1293	78	5.6	416	1	OX1R	MOUSE	P58307	mus musculu	1366	77.5	5.6	288	2	Q3B0R8	SYNS9	Q3b0r8	synecococc
1294	78	5.6	416	2	Q5FLR6	LACAC	Q5flr6	lactobacill	1367	77.5	5.6	291	2	Q4HPK2	CAMUP	Q4hpk2	campylobact
1295	78	5.6	421	2	Q2Z672	CABEL	Q2z672	caenorhabdi	1368	77.5	5.6	291	2	Q6ASD9	DESPS	Q6asd9	desulfotale
1296	78	5.6	424	2	Q6SFZ8	9BACT	Q6sfz8	uncultured	1369	77.5	5.6	292	2	Q4EK11	LISMO	Q4ek11	listeria mo
1297	78	5.6	427	2	Q421Y0	DESHA	Q421y0	desulfitoba	1370	77.5	5.6	292	2	Q721V7	LISMF	Q721v7	listeria mo
1298	78	5.6	428	2	Q6LS34	PHOPR	Q6ls34	photobacter	1371	77.5	5.6	293	2	Q2XBL5	PSEPU	Q2xbl5	pseudomonas
1299	78	5.6	429	2	Q4LAB4	STAHT	Q4lab4	staphylococ	1372	77.5	5.6	293	2	Q88E98	PSEPK	Q88e98	pseudomonas
1300	78	5.6	449	2	Q4HES6	CAMCO	Q4hes6	campylobact	1373	77.5	5.6	293	2	Q8ZGV5	YERPE	Q8zgv5	yersinia pe
1301	78	5.6	449	2	Q4HIV2	CAMLA	Q4hiv2	campylobact	1374	77.5	5.6	296	2	Q33U75	9GAMM	Q33u75	shewanella
1302	78	5.6	452	2	Q7VAQ3	PROMA	Q7vaq3	prochloroco	1375	77.5	5.6	296	2	Q92ZH0	RHIME	Q92zh0	rhizobium m
1303	78	5.6	459	2	Q3BEN3	9FALC	Q3ben3	spizaetux a	1376	77.5	5.6	297	2	Q2JX36	9CYAN	Q2jx36	cyanobacter
1304	78	5.6	462	2	Q9V8L1	PYRFU	Q9v8l1	pyrococcus	1377	77.5	5.6	300	2	Q31U75	SHIBS	Q31u75	shigella bo
1305	78	5.6	467	2	Q95JD3	RABIT	Q95jd3	oryctolagus	1378	77.5	5.6	308	2	Q660J1	BORGA	Q660j1	borrelia ga
1306	78	5.6	470	2	Q3JCK0	NITOC	Q3jck0	nitrosococ	1379	77.5	5.6	312	2	Q7TR57	MOUSE	Q7tr57	mus musculu
1307	78	5.6	474	2	Q3XX38	ENTFC	Q3xx38	enterococ	1380	77.5	5.6	312	2	Q8VG20	MOUSE	Q8vg20	mus musculu
1308	78	5.6	474	2	Q8GGM7	STRAZ	Q8ggm7	streptomyce	1381	77.5	5.6	313	2	Q7TSS3	MOUSE	Q7tss3	mus musculu
1309	78	5.6	476	2	Q2WYS7	9GAMM	Q2wys7	shewanella	1382	77.5	5.6	317	2	Q8RFU5	FUSNN	Q8rfu5	fusobacteri
1310	78	5.6	484	2	Q33J33	METHU	Q33j33	methanospir	1383	77.5	5.6	318	1	NU1M	VARRU	NU1M	varanus rud
1311	78	5.6	486	2	Q8EKR6	SHEON	Q8ekr6	shewanella	1384	77.5	5.6	321	2	Q94V72	VARGI	Q94v72	varanus gig
1312	78	5.6	486	2	Q68714	MOUSE	Q68714	mus musculu	1385	77.5	5.6	321	2	Q9MR26	9MYRT	Q9mr26	comolia cor
1313	78	5.6	490	2	Q8FP18	COREF	Q8fp18	corynebacte	1386	77.5	5.6	327	2	Q9MR26	9MYRT	Q9mr26	comolia cor
1314	78	5.6	495	2	Q6R9L4	MAIZE	Q6r9l4	zea mays (m	1387	77.5	5.6	333	2	Q3D2B9	STRAG	Q3d2b9	streptococ
1315	78	5.6	498	2	Q8BVS0	MOUSE	Q8bvs0	mus musculu	1388	77.5	5.6	335	2	Q9X0N3	9CETA	Q9x0n3	thermotoga
1316	78	5.6	511	2	Q2JPR0	9CYAN	Q2jpr0	cyanobacter	1389	77.5	5.6	347	2	Q70RW1	9CETA	Q70rw1	berardius b
1317	78	5.6	517	2	Q98H22	RHILO	Q98h22	rhizobium l	1390	77.5	5.6	354	2	Q2UTW7	ASFOR	Q2utw7	aspergillus
1318	78	5.6	521	2	Q3GE78	9GAMM	Q3ge78	shewanella	1391	77.5	5.6	359	2	Q38FV3	9RYRP	Q38fv3	trypanosoma
1319	78	5.6	526	2	Q47B84	DECAR	Q47b84	dechloromon	1392	77.5	5.6	359	2	Q6GDS8	STAAR	Q6gds8	staphylococ
1320	78	5.6	533	2	Q3SHA8	9BRAD	Q3sha8	bradyrhizob	1393	77.5	5.6	363	2	Q9YF04	ASRPE	Q9yfu4	aeropyrum p
1321	78	5.6	537	2	Q3JX86	BURP1	Q3jx86	burkholderi	1394	77.5	5.6	367	2	Q67RR1	SWMTH	Q67rr1	syndiobacte
1322	78	5.6	538	2	Q9JAE1	9PARA	Q9jae1	mumps virus	1395	77.5	5.6	368	2	Q85GB7	9DIPS	Q85gb7	cryptothlad
1323	78	5.6	540	2	Q54IV7	DICDI	Q54iv7	dictyosteli	1396	77.5	5.6	370	2	Q4D715	TRYCR	Q4d715	trypanosoma
1324	78	5.6	551	2	Q8BKG6	MOUSE	Q8bwg6	m o day neo	1397	77.5	5.6	372	2	Q5AQX4	EMENI	Q5aqx4	aspergillus
1325	78	5.6	553	2	Q6CQ66	KLUJA	Q6cq66	kluveromyce	1398	77.5	5.6	386	2	Q4ZR77	PSEU2	Q4zr77	pseudomonas
1326	78	5.6	554	2	Q34FM4	RHOPA	Q34fm4	rhodopseud	1399	77.5	5.6	386	2	Q3SHL0	THIDA	Q3shl0	thiobacillu
1327	78	5.6	554	2	Q6NAP5	RHOPA	Q6nap5	rhodopseud	1400	77.5	5.6	389	2	Q3QE50	9GAMM	Q3qe50	shewanella
1328	78	5.6	560	2	Q467V6	METBA	Q467v6	methanosarc	1401	77.5	5.6	398	2	Q57PC1	SALCH	Q57pc1	salmonella
1329	78	5.6	565	2	Q9F3S8	RHOWR	Q9f3s8	rhodothermu	1402	77.5	5.6	399	2	Q78I12	THEVO	Q78i12	thermoplasm
1330	78	5.6	573	2	Q72LX4	LEPIC	Q72lx4	leptospira	1403	77.5	5.6	406	2	Q6DNG7	SOYBN	Q6dng7	glycine max
1331	78	5.6	574	2	Q72T06	LEPIC	Q72t06	leptospira	1404	77.5	5.6	406	2	Q4JZ96	STRPN	Q4jz96	streptococ
1332	78	5.6	581	2	Q8FZFB	LEFIN	Q8fzfb	leptospira	1405	77.5	5.6	425	2	Q3GK04	CHLVI	Q3gk04	prosthecoch
1333	78	5.6	581	2	Q59TF8	CANAL	Q59tf8	candida alb	1406	77.5	5.6	436	2	Q8F6X7	BRARE	Q8f6x7	brachydanio
1334	78	5.6	581	2	Q59TR0	CANAL	Q59tr0	candida alb	1407	77.5	5.6	438	2	Q33TM7	9GAMM	Q33tm7	shewanella
1335	78	5.6	585	2	Q59MN0	CANAL	Q59mn0	candida alb	1408	77.5	5.6	443	2	Q8TRL4	METAC	Q8trl4	methanosarc
1336	78	5.6	587	2	Q4ZL77	PSEU2	Q4zl77	pseudonabdi	1409	77.5	5.6	446	2	Q4NIJ1	9MICC	Q4ni1j	arthrobacte
1337	78	5.6	590	2	Q01843	CABEL	Q01843	caenorhabdi	1410	77.5	5.6	448	2	Q2UR20	ASFOR	Q2ur20	aspergillus
1338	78	5.6	650	2	Q6XJL1	9ERIC	Q6xjl1	neolemonnie	1411	77.5	5.6	448	2	Q9XMU9	TETPY	Q9xmu9	tetrachymena
1339	78	5.6	659	2	Q5JB71	9ASPA	Q5jb71	babiana muc	1412	77.5	5.6	453	2	Q3CX85	ALTAT	Q3cx85	pseudalter
1340	78	5.6	662	2	Q4K7U5	PSEF5	Q4k7u5	pseudomonas	1413	77.5	5.6	458	2	Q6CZJ3	ERWCT	Q6czj3	erwinia car
1341	78	5.6	672	2	Q5JBA6	9ASPA	Q5jba6	scaadoxus ci	1414	77.5	5.6	459	2	Q85UJ5	COTCH	Q85uj5	coturnix ch
1342	78	5.6	694	2	Q95677	SOLDU	Q95677	solanum dul	1415	77.5	5.6	460	2	Q7N370	PHOLL	Q7n370	photorhabdu
1343	78	5.6	806	2	Q4P678	USTMA	Q4p678	ustilago ma	1416	77.5	5.6	461	2	Q8X7F9	ECO57	Q8x7f9	escherichia
1344	78	5.6	808	2	Q50V14	ENTHI	Q50v14	entamoeba h	1417	77.5	5.6	464	2	Q916G9	PSEAE	Q916g9	pseudomonas
1345	78	5.6	830	2	Q8PQ48	XANAC	Q8pq48	xanthomonas	1418	77.5	5.6	472	2	Q2WRP4	CLOBE	Q2wrp4	clostridium

1419	77.5	5.6	477	2	Q7MKV7_VIBVY	Q7mkv7 vibrio vuln
1420	77.5	5.6	477	2	Q87PF8_VIBPA	Q87pf8 vibrio para
1421	77.5	5.6	477	2	Q8D911_VIBVU	Q8d911 vibrio vuln
1422	77.5	5.6	479	2	Q7AEJ3_ECO57	Q7aej3 escherichia
1423	77.5	5.6	481	2	Q3QNW1_9RHOB	Q3qnw1 silicibacte
1424	77.5	5.6	481	2	Q2SJS3_9GAMW	Q2sj33 hahella che
1425	77.5	5.6	483	2	Q5KYK3_GEOKA	Q5kyk3 geobacillus
1426	77.5	5.6	483	2	Q2U0J8_ASPOR	Q2u0j8 aspergillus
1427	77.5	5.6	484	2	Q4CDC2_CLOTM	Q4cdc2 clostridium
1428	77.5	5.6	482	2	Q7VPT5_HELHP	Q7vpt5 helicobacte
1429	77.5	5.6	489	2	Q57JZ0_SALCH	Q57jz0 salmonella
1430	77.5	5.6	489	2	Q82363_SALTI	Q82363 salmonella
1431	77.5	5.6	500	2	Q2K5A6_RHIET	Q2k5a6 rhizobium e
1432	77.5	5.6	504	2	Q68816_ORYSA	Q68816 oryza sativ
1433	77.5	5.6	507	2	Q7V8Q9_BORPE	Q7v8q9 bordetella
1434	77.5	5.6	507	2	Q7WDH8_BORBR	Q7wdh8 bordetella
1435	77.5	5.6	510	1	X382_RICPR	Q9zde9 rickettsia
1436	77.5	5.6	510	2	Q9LE20_ARATH	Q9le20 arabidopsis
1437	77.5	5.6	510	2	Q4MX86_BACCE	Q4mx86 bacillus ce
1438	77.5	5.6	513	2	Q9KLS4_VIBCH	Q9kl84 vibrio chol
1439	77.5	5.6	520	2	Q32477_JUSAM	Q32477 justicia am
1440	77.5	5.6	524	2	Q458G9_9BURK	Q458g9 burkholderi
1441	77.5	5.6	524	2	Q4L9V5_9BURK	Q4l9v5 burkholderi
1442	77.5	5.6	526	1	STP13_ARATH	Q94az2 arabidopsis
1443	77.5	5.6	526	2	Q55WR7_CRYNE	Q55wr7 cryptococcu
1444	77.5	5.6	526	2	Q5KJ10_CRYNE	Q5kj10 cryptococcu
1445	77.5	5.6	527	2	Q5ATG4_EMENI	Q5atg4 aspergillus
1446	77.5	5.6	531	2	Q6Y0U3_ONYPE	Q6y0u3 onion yello
1447	77.5	5.6	532	1	COX1_RHOCA	P98059 rhodobacter
1448	77.5	5.6	532	2	Q40HU4_9RHOB	Q40hu4 jannaschia
1449	77.5	5.6	535	2	Q55577_SYNY3	Q55577 synechocyst
1450	77.5	5.6	558	2	Q43ZK5_SOLUS	Q43zk5 solibacter
1451	77.5	5.6	612	2	Q76HH6_KATPE	Q76hh6 katusonus
1452	77.5	5.6	612	2	Q85UE1_9SCOM	Q85ue1 eutymnus a
1453	77.5	5.6	616	2	Q3XM94_9PROT	Q3xm94 magnetococ
1454	77.5	5.6	617	2	Q7S080_NEUCR	Q7s080 neurospora
1455	77.5	5.6	630	1	SC6A4_MACMU	Q9myx0 macaca mula
1456	77.5	5.6	635	2	Q9AS87_ARATH	Q9aes7 arabidopsis
1457	77.5	5.6	639	2	Q85LH6_PISOC	Q85lh6 pisaster oc
1458	77.5	5.6	643	2	Q385G4_9TRYP	Q385g4 trypanosoma
1459	77.5	5.6	648	2	Q8SLR2_COUGU	Q8slr2 couroupita
1460	77.5	5.6	649	2	Q28449_ARCFU	Q28449 archaeoglob
1461	77.5	5.6	660	2	Q6YIT3_9LILI	Q6yit3 lachnanthes
1462	77.5	5.6	665	2	Q9GGT9_9POAL	Q9ggt9 dulichium a
1463	77.5	5.6	695	2	Q97A18_THEVO	Q97a18 thermoplasm
1464	77.5	5.6	698	2	Q6BZ22_DEBHA	Q6bz22 debaryomyc
1465	77.5	5.6	699	2	Q7YM04_9SOLA	Q7ym04 metternichy
1466	77.5	5.6	706	2	Q6MK05_DDEBA	Q6mk05 bdellovibri
1467	77.5	5.6	717	1	PAL2_ARATH	P45724 arabidopsis
1468	77.5	5.6	750	2	Q93S90_XANCP	Q93s90 xanthomonas
1469	77.5	5.6	776	2	Q61N20_CABER	Q61nz0 caenorhabdi
1470	77.5	5.6	821	2	Q4CY87_TRYCR	Q4cy87 trypanosoma
1471	77.5	5.6	839	2	Q8T074_METAC	Q8tq74 methanosarc
1472	77.5	5.6	855	2	Q75AV9_ASHGO	Q75av9 ashbya goss
1473	77.5	5.6	861	2	Q89FW4_BRAJA	Q89fw4 bradyrhizob
1474	77.5	5.6	870	1	Q61555_HUMAN	Q7z3f1 homo sapien
1475	77.5	5.6	870	2	Q4GOV6_HUMAN	Q4gov6 homo sapien
1476	77.5	5.6	877	2	Q2SB79_HABEL	Q2sb79 hahella che
1477	77.5	5.6	881	2	Q31LG1_PSEHT	Q31lg1 pseudoalter
1478	77.5	5.6	945	1	SYI_ACTAD	Q6fg02 acinetobact
1479	77.5	5.6	953	1	CMH43_YEAST	P25618 saccharomyc
1480	77.5	5.6	1069	2	Q41VA6_AZOVI	Q41va6 azotobacter
1481	77.5	5.6	1118	2	Q9HUE7_PSEAE	Q9hue7 pseudomonas
1482	77.5	5.6	1402	1	K02322_HUMAN	Q92628 homo sapien
1483	77.5	5.6	1551	2	Q44718_SOLUS	Q44718 solibacter
1484	77.5	5.6	1646	2	Q5B0U5_EMENI	Q5bou5 aspergillus
1485	77	5.5	175	2	Q3A0L5_PELCD	Q3a0l5 pelobacter
1486	77	5.5	181	2	Q8ZU94_PYRAE	Q8zu94 pyrobaculum
1487	77	5.5	228	1	CRCB_METCA	Q60sp3 methylococ
1488	77	5.5	262	2	Q8KJ17_RHILO	Q8kj17 rhizobium l
1489	77	5.5	268	2	Q35LN3_9BRAD	Q35ln3 bradyrhizob
1490	77	5.5	269	2	Q4B819_BURVI	Q4b819 burkholderi
1491	77	5.5	269	2	Q393M5_BUR33	Q393m5 burkholderi

ALIGNMENTS

RESULT 1

Q6UX65_HUMAN	PRELIMINARY;	PRT;	266 AA.
ID	Q6UX65_HUMAN	PRELIMINARY;	PRT; 266 AA.
AC	Q6UX65; Q86VD3;		
DT	05-JUL-2004,	integrated into UniProtKB/TrEMBL.	
DT	05-JUL-2004,	sequence version 1.	
DT	07-FEB-2006,	entry version 13.	
DE	WF0154 (Hypochemical protein TMEM77) (Novel protein).		
GN	Name=TMEM77; Synonyms=RP5-1180E21.1; ORFNames=RP5-1180E21.1-001,		
GN	UNQ154;		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;		
OC	Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	NCLEOTIDE SEQUENCE.		
RX	MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;		
RA	Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,		
RA	Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,		
RA	Eaton D., Foster J.S., Grimaldi C., Gu Q., Hass P.E., Heldens S.,		
RA	Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,		
RA	Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J.,		
RA	Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,		
RA	Vandlen R.L., Watanabe C., Wieand D., Woods K., Xie M.-H.,		
RA	Yanura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,		
RA	Wood W.I., Godowski P.J., Gray A.M.,		
RT	"The secreted protein discovery initiative (SPDI), a large-scale		
RT	effort to identify novel human secreted and transmembrane proteins: a		
RT	bioinformatics assessment."		
RN	Genome Res. 13:2265-2270(2003).		
RP	NCLEOTIDE SEQUENCE.		
RC	TISSUE=Brain, and Eye;		
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;		
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,		
RA	Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,		
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,		
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,		
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,		
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,		
RA	Raha S.S., Locquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,		
RA	Rosa S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,		
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,		
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,		
RA	Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,		
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,		
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,		
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,		
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,		
RA	Schmurch A., Schein J.E., Jones S.J.M., Marra M.A.,		
RT	"Generation and initial analysis of more than 15,000 full-length human		
RT	and mouse cDNA sequences."		
RN	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).		
RP	NCLEOTIDE SEQUENCE.		
RC	TISSUE=Eye;		
RN	[3]		
RP	NCLEOTIDE SEQUENCE.		
RC	NIH MGC Project;		

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RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE.
RA Thomas D.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RG NIH MGC Project;
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; AY358492; AAQ8856.1; -; mRNA.
DR EMBL; BC047025; AAH47025.3; -; mRNA.
DR EMBL; AL355816; CAI19366.1; -; Genomic DNA.
DR EMBL; BC091509; AAH91509.1; -; mRNA.
DR Ensembl; ENSG00000156171; Homo sapiens.
KW Hypothetical protein.
SQ SEQUENCE 266 AA; 29766 MW; 4F91D5C212D459E5 CRC64;

Query Match 100.0%; Score 1392; DB 2; Length 266;
Best Local Similarity 100.0%; Pred. No. 6e-108;
Matches 266; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MWFFQGLSFLPSALVIWTSAAFIYSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAML 60
DB 1 MWFFQGLSFLPSALVIWTSAAFIYSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAML 60
QY 61 NIAAALCIATIVYRYKQVHALSPENVIKLNKAGLVGLSCLGLSIVANFQKTLTFAA 120
DB 61 NIAAALCIATIVYRYKQVHALSPENVIKLNKAGLVGLSCLGLSIVANFQKTLTFAA 120
QY 121 HVSGAVLTFGMSLYMFVQTILSYQMPKIHGKQVFWIRLLLVICGVSALSMLTCSYVL 180
DB 121 HVSGAVLTFGMSLYMFVQTILSYQMPKIHGKQVFWIRLLLVICGVSALSMLTCSYVL 180
QY 181 HSGNFGTDLQKLNHPEDKGYVLHMITTAAEWSMSFSFGPFLTYIRDFQKISLRVEAN 240
DB 181 HSGNFGTDLQKLNHPEDKGYVLHMITTAAEWSMSFSFGPFLTYIRDFQKISLRVEAN 240
QY 241 LHGLTLYDTAPCPINNERTLLSRDI 266
DB 241 LHGLTLYDTAPCPINNERTLLSRDI 266

RESULT 3
Q3ZC48_BOVIN PRELIMINARY; PRT; 266 AA.
ID Q3ZC48_BOVIN
AC Q3ZC48;
DT 27-SEP-2005, integrated into UniProtKB/TrEMBL.
DT 27-SEP-2005, sequence version 1.
DT 07-MAR-2006, entry version 5.
DE Hypothetical protein.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Hereford; TISSUE=Rumen;
RA Moore S., Alexander L., Brownstein M., Guan L., Lobo S., Meng Y.,
RA Tanaguchi M., Wang Z., Yu J., Prange C., Schreiber K., Shennen C.,
RA Wagner L., Balla M., Barbazuk S., Barber S., Babakaiff R., Beland J.,
RA Chun E., Del Rio L., Gibson S., Hanson R., Kirkpatrick R., Liu J.,
RA Matsuo C., Mayo M., Santos R.R., Stott J., Tsai M., Wong D.,
RA Siddiqui A., Holt R., Jones S.J., Marra M.A.;
RL Submitted (AUG-2005) to the EMBL/GenBank/DBJ databases.
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CC -----
KW Hypothetical protein.
DR EMBL; BC102918; AA102919.1; -; mRNA.
SQ SEQUENCE 266 AA; 29923 MW; A3A00ECE27834855 CRC64;

Query Match 93.0%; Score 1295; DB 2; Length 266;
Best Local Similarity 90.2%; Pred. No. 7.6e-100;
Matches 240; Conservative 15; Mismatches 11; Indels 0; Gaps 0;

QY 1 MWFFQGLSFLPSALVIWTSAAFIYSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAML 60
DB 1 MWFFQGLSFLPSALVIWTSAAFIYSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAML 60
QY 61 NIAAALCIATIVYRYKQVHALSPENVIKLNKAGLVGLSCLGLSIVANFQKTLTFAA 120
DB 61 NIAAALCIATIVYRYKQVHALSPENVIKLNKAGLVGLSCLGLSIVANFQKTLTFAA 120
QY 121 HVSGAVLTFGMSLYMFVQTILSYQMPKIHGKQVFWIRLLLVICGVSALSMLTCSYVL 180
DB 121 HVSGAVLTFGMSLYMFVQTILSYQMPKIHGKQVFWIRLLLVICGVSALSMLTCSYVL 180
DB 121 HVCGAVLTFGMSLYMFVQTILSYQMPKIHGKQVFWIRLLLVICGVSALSMLTCSYVL 180

Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
[4]
NUCLEOTIDE SEQUENCE.
Thomas D.;
Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
[5]
NUCLEOTIDE SEQUENCE.
TISSUE=Brain;
NIH MGC Project;
Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
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DR EMBL; AY358492; AAQ8856.1; -; mRNA.
DR EMBL; BC047025; AAH47025.3; -; mRNA.
DR EMBL; AL355816; CAI19366.1; -; Genomic DNA.
DR EMBL; BC091509; AAH91509.1; -; mRNA.
DR Ensembl; ENSG00000156171; Homo sapiens.
KW Hypothetical protein.
SQ SEQUENCE 266 AA; 29766 MW; 4F91D5C212D459E5 CRC64;

Query Match 100.0%; Score 1392; DB 2; Length 266;
Best Local Similarity 100.0%; Pred. No. 6e-108;
Matches 266; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MWFFQGLSFLPSALVIWTSAAFIYSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAML 60
DB 1 MWFFQGLSFLPSALVIWTSAAFIYSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAML 60
QY 61 NIAAALCIATIVYRYKQVHALSPENVIKLNKAGLVGLSCLGLSIVANFQKTLTFAA 120
DB 61 NIAAALCIATIVYRYKQVHALSPENVIKLNKAGLVGLSCLGLSIVANFQKTLTFAA 120
QY 121 HVSGAVLTFGMSLYMFVQTILSYQMPKIHGKQVFWIRLLLVICGVSALSMLTCSYVL 180
DB 121 HVSGAVLTFGMSLYMFVQTILSYQMPKIHGKQVFWIRLLLVICGVSALSMLTCSYVL 180
QY 181 HSGNFGTDLQKLNHPEDKGYVLHMITTAAEWSMSFSFGPFLTYIRDFQKISLRVEAN 240
DB 181 HSGNFGTDLQKLNHPEDKGYVLHMITTAAEWSMSFSFGPFLTYIRDFQKISLRVEAN 240
QY 241 LHGLTLYDTAPCPINNERTLLSRDI 266
DB 241 LHGLTLYDTAPCPINNERTLLSRDI 266

RESULT 2
Q4VWF6_HUMAN PRELIMINARY; PRT; 266 AA.
ID Q4VWF6_HUMAN
AC Q4VWF6;
DT 05-JUL-2005, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE Putative transmembrane protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Xu J., Xie Y., Mao Y.;
RT "Identification of a novel human putative transmembrane protein that
RT is up-regulated in hepatoma.";
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; AY336747; AAR02410.1; -; mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
KW Transmembrane.
```


Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-P., Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S., Hayashizaki Y.;
Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
[6]
RL NUCLEOTIDE SEQUENCE.
RN
RP STRAIN=C57BL/6J; TISSUE=Testis;
RC MEDLINE=20499374; PubMed=11042125; DOI=10.1101/gr.145100;
RX MEDLINE=20499374; PubMed=11042125;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN
RP NUCLEOTIDE SEQUENCE.
RN
RP STRAIN=C57BL/6J; TISSUE=Testis;
RC MEDLINE=2030913; PubMed=11076861; DOI=10.1101/gr.152600;
RX MEDLINE=2030913; PubMed=11076861;
RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-Format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN
RP NUCLEOTIDE SEQUENCE.
RN
RP STRAIN=C57BL/6J; TISSUE=Testis;
RC ADACHI J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shingagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Teijima Y., Toyota T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
CC
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CC Distributed under the Creative Commons Attribution-NoDerivs License
CC
CC EMBL: AK015888; BAB30020.1; -; mRNA.
DR Ensembl: ENSMUSG00000027900; Mus musculus.
DR MGI: MGI:1914421; 2610318G18R1K.
DR
SQ SEQUENCE 267 AA; 30244 MW; 228214DSAFF37CFB CRC64;
Query Match 88.7%; Score 1235; DB 2; Length 267;
Best Local Similarity 86.0%; Pred. No. 7.8e-95;
Matches 228; Conservative 19; Mismatches 18; Indels 0; Gaps 0
QY 1 MWMFQGLSFLPSALVIVTSAAFISYITAVTLHHIDPALPYISDTGTVAPEKCLFGAML 60
Db 1 MWMFQGLSFLPSALVIVTFAITFISYITATLHHVDPALPYISDTGTIPERCLFGVML 60
QY 61 NTAALVLCATITVYRVKQVHALSPENVIIKLNKAGLVIGILSCILGISLVANFOKTLTPAA 120
Db 61 NTAALVGIATVYRVKQVHALNPENLIKLNKAGLVIGILSCILGISLVANFOKSTLFTV 120
QY 121 HVSGLVLTFGMGSGLYMFQVITLSYQMPKIRHGKQVFWIRLLLVTCGVSALSMLTCSVSL 180
Db 121 HVCGLVLAEPMSGSGFTAFVQTILSYQMPKIRHSQVFWIRLLLVTCGVSALSMLTCSVSL 180
QY 181 HSGNFGTDLQKHLWNPKDGKYLHMTTAAEWSMSFSFFGFFITYIRDPQKISLRVEAN 240
Db 181 YSSDFGPDVVOKHLWNPKDGKYLHMTTAAEWSMSFSFFGFFITYIRDPQKISLRVEAN 240

241 LHGLTLYDTAPCPINNETRLLSRD 265
||||| ||||| ||||| ||||| ||||| |||||
241 LHGLTLYDTPCLVNNETRLLSRD 265

RESULT 7

Q9D835_MOUSE PRELIMINARY; PRT; 180 AA.
Q9D835;
AC 01-JUN-2001, integrated into UniprotKB/TREMBL.
DT 01-JUN-2001, sequence version 1.
DT 07-FEB-2006, entry version 22.
DE Adult male small intestine cDNA, RIKEN full-length enriched library,
DE clone:2010305N14 product:RIKEN CDNA 2010305N14 (Hypothetical protein
DE Tmem77).
DE Name=2610318G18Rik; Synonyms=Tmem77;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Small intestine;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.
RT "High-efficiency full-length cDNA cloning.";
RL Methods Enzymol. 303:19-44(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Small intestine;
RX PubMed=16141072; DOI=10.1126/science.1112014;
RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA Bajic V.B., Bremner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA Davis M.J., Wilming L.G., Aidinis V., Allen J.B.,
RA Bansal M., Baxter L., Bewell K.W., Bersano T., Bono H., Chalk A.M.,
RA Bangesi-Mpimbato A., Peisler K., Atturaliya R.N., Bailey T.L.,
RA Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
RA di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,
RA Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
RA Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
RA Gustinctch S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
RA Hall D., Huminiecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
RA Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
RA Kitano H., Kollias G., Kriehnan S.P., Kruger A., Kummerfeld S.K.,
RA Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
RA Luoni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
RA Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
RA Motteguir-Tabar S., Mulder N., Nakano N., Nakachi H., Ng P.,
RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
RA Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavese G., Pesole G.,
RA Petrovsky N., Piazza S., Read J., Reid J.F., Ring B.Z., Ringwald M.,
RA Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
RA Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
RA Sperling S., Stupka E., Sugtara K., Sultana R., Takenaka Y., Taki K.,
RA Tamojia K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
RA Ueda H.R., van Nimwegen B., Verardo R., Wei C.L., Yagi K.,
RA Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
RA Grimmond S.M., Tesardale R.D., Liu E.T., Brusic V., Quackenbush J.,
RA Wahlstedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
RA Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
RA Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Nimomiya N.,
RA Nishio T., Okada M., Plessey C., Shibata K., Shiraki T., Suzuki S.,
RA Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
RA Hayashizaki Y.;
RT "The transcriptional landscape of the mammalian genome.";
RL Science 309:1559-1563 (2005).
RN [3]
RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Small intestine;
 RX PubMed=16141073; DOI=10.1126/science.11112009;
 RG RIKEN Genome Exploration Research Group, and Genome Science Group
 (Genome Network Core Team) and the FANTOM Consortium;
 RT "Antisense Transcription in the Mammalian Transcriptome";
 RL Science 309:1564-1566(2005).
 RN [14]

RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Small intestine;
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikaido I., Ootani N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.P., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 RA Ravasi T., Reed J.C., Reid D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wyshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavalan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
 RA Shizaki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.;
 RA "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs";
 RL Nature 420:563-573(2002).
 RN [5]

RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Small intestine;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukuuchi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Glessi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bono M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection";
 RL Nature 409:685-690(2001).
 RN [6]

RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Small intestine;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes";
 RL Genome Res. 10:1617-1630(2000).
 RN [7]

RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Small intestine;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Katsunai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multiplexed capillary sequencer";
 RL Genome Res. 10:1757-1771(2000).
 RN [8]

RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Small intestine;
 RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
 RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukuishi Y., Furuno M.,
 RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
 RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
 RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
 RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
 RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
 RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
 RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
 RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
 RA Muramatsu M., Hayashizaki Y.;
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 RN [9]

RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=FVB/N; TISSUE=Kidney;
 RX MEDLINE=2338257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Klausner R.D., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins P.S., Wagner L., Sherman C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Busto K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marasina K., Farmer A., Rubin G.M., Hong L.,
 RA Diatchenko L., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Robak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettner M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Myers D.E.,
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Marra M.A.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [10]

RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=FVB/N; TISSUE=Kidney;
 RG NIH MGC Project;
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.

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Query Match 57.9%; Score 805.5; DB 2; Length 180;
 Best Local Similarity 60.0%; Pred. No. 3.8e-59;
 Matches 159; Conservative 12; Mismatches 7; Indels 87; Gaps 1;
 QY 1 MWFFQGLSFLPSALVIVTSAAFISYITAVTLHHIDPALPIYSDTGTVAPEKCLFGAML 60
 DB 1 MWFFQGLSFLPSALVIVTSAAFISYITAVTLHHIDPALPIYSDTGTVAPEKCLFGAML 60
 QY 61 NIAAVLCIATYVRYKQVHALSPENVIKLKGVLGILSCILSVANFQKTLTFAA 120
 DB 61 NIAAVLCIATYVRYKQVHALSPENVIKLKGVLGILSCILSVANFQKTLTFAA 120

RESULT 8

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241 ELQSNHLYES 250
|||:
Db

RESULT 9
Q8NEQ4 HUMAN Q8NEQ4 HUMAN PRELIMINARY; PRT; 136 AA.
AC Q8NEQ4;
DT 01-OCT-2002, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2002, sequence version 1.
DT 07-MAR-2006, entry version 12.
DE CDNA PSEC0031 fis, clone NT2RP1000593.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OC NCBI_TaxID=9606;
[1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=1630743; DOI=10.1093/dnares/12.2.117;
RA Otsuki T., Oca T., Nishikawa T., Hayashi K., Suzuki Y., Yamamoto J.,
RA Wakamatsu A., Kimura K., Sakamoto K., Hatano N., Kawai Y., Ishii S.,
RA Saito K., Kojima S., Sugiyama T., Ono T., Okano K., Yoshikawa Y.,
RA Aotsuka S., Sasaki N., Hattori A., Okumura K., Nagai K., Sugano S.,
RA Iseaga T.;
RT "Signal sequence and keyword trap in silico for selection of full-
RT length human cDNAs encoding secretion or membrane proteins from oligo-
RT capped cDNA libraries.";
RL DNA Res. 12:117-126(2005).
-----
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-----
EMBL; AK075350; BAC11562.1; -; mRNA.
Ensembl; ENSG00000156171; Homo sapiens.
SO SEQUENCE 136 AA; 15728 MW; 984FEDC29636AC0C CRC64;

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Query Match	52.1%	Score 725	DB 2	Length 136
Best Local Similarity	100.0%	Pred. No. 1.5e-52		
Matches 136	Conservative 0	Mismatches 0	Indels 0	Gaps 0
Qy	131	MGSLYMFVQTILSYQMCPKIHGKQVFWIRLLLVICWGSVALSMLTCSSVLHSGNFGTDLE	190	
Db	1	MGSLYMFVQTILSYQMCPKIHGKQVFWIRLLLVICWGSVALSMLTCSSVLHSGNFGTDLE	60	
Qy	191	QKLHWNPEDKGYVLHMTTAAEWSMSFSFGFFLTYIRDPQKISURVEANLHGLTLYDTA	250	
Db	61	QKLHWNPEDKGYVLHMTTAAEWSMSFSFGFFLTYIRDPQKISURVEANLHGLTLYDTA	120	
Qy	251	PCPINNERTLLSRDI	266	
Db	121	PCPINNERTLLSRDI	136	

RESULT 10
QSN682 HUMAN
ID Q8N682 HUMAN
AC Q8N682;
PRELIMINARY; PRT; 238 AA.

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DT 01-OCT-2002, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2002, sequence version 1.
DT 07-FEB-2006, entry version 16.
DE FLJ1259 protein.
GN Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rutterfield Y.S.N., Krzywicki M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Liver;
RC Director MGC Project;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; BC018435; AAH18435.1; -; mRNA.
DR Ensembl; ENSG00000136048; Homo sapiens
SQ SEQUENCE 238 AA; 26253 MW; 51187567737F6C0 CRC64;

Query Match - 35.4%; Score 492.5; DB 2; Length 238;
Best Local Similarity 38.8%; Pred. NO. 7e-33;
Matches 97; Conservative 53; Mismatches 79; Indels 21; Gaps 3;

QY 1 MHWFOGLSFLPSALVIVTWSAIFSYITAVTLHIDPALPYISDTGTVAPEKCLFGAML 60
DB 1 MLCFLRGMAFVPLLLTWSSAIFSYVAVLSGHVNPFLPYISDTGTTPPSGIFGFWI 60

QY 61 NIAAVLCIATIVRYKQV-----HALSPENVIKLNKAGLVGLISLGVANFQ 113
DB 61 NFSAFGANTWTRYKIVQKQNTCYFSTFVFNLV-----SLVLGVCFCFGVIANFQ 114

QY 114 KTTLPAAHVSAGVLTFGMSGLYMFVQTILSYQMPKHQGVFWIRLLVIVGVSALSM 173
DB 115 ELAVPVVHDGALLAPVCGVYVTLQSIISYKSCPQWNSLSTCHIRWISAVSCAAVPM 174

QY 174 LTCSSVLHSGNFTDLEQKLNWPKGVVLHMITTAEWMSFSFSGFGLYIRDFQKI 233
DB 175 IVCASLISI-----TKLEWNPREDKYVHVVSACIEWTVAFGFIFVFLFIQDFQSV 226

QY 234 SLRVEANLHG 243
DB 227 TLRISTEING 236

RESULT 11
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RA NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01286;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Kongsaya A., Kurochik I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shinada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlstedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sakaki D., Shibata K., Shingawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs";
RL Nature 420:563-573 (2002).
[5]
RA NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
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RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
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RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
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RT "Functional annotation of a full-length mouse cDNA collection";
RL Nature 409:685-690 (2001).
[6]
RA NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes";
RL Genome Res. 10:1617-1630 (2000).
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RA NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitesunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,

RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
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RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multiplexed capillary sequencer";
RL Genome Res. 10:1757-1771 (2000).
[8]
RA NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=20578163; PubMed=11042159; DOI=10.1101/gr.145100;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
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RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shingawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2000) to the ENBL/GenBank/DBJ databases.
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CC
CC EMBL: AK004552; BAB23366.2; -: mRNA.
DR Ensembl: ENSMUSG00000020057; Mus musculus.
DR MGI: MGI:1918962; 1200002N14Rik.
DR GO: GO:0003676; P:nucleic acid binding; RCA.
KW Hypothetical protein.
SQ SEQUENCE 238 AA; 26201 MW; AC89F1301B0A0048 CRC64;
Query Match 34.4%; Score 479.5; DB 2; Length 238;
Best Local Similarity 37.3%; Pred. No. 8.5e-32; Indels 21; Gaps 3;
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DB 1 MLCFLRGNAFVFLVLTWSSAAFIYSYVAVLSGHVNFYISDTGTTPESGIFGFWI 60
QY 61 NIAAVLCIATYVRYKQV-----HALSPENVIKLNKAGLVGLISGLSIVANFQ 113
DB 61 NFSALPGAATWYTRYKIVKQNETCYFSTPVFNLV-----SLALGLVCGIGMGIVANFQ 114
QY 114 KTTLPAAHVSGAVLTFGMSLYMFVQTILSYQMPKIHGQVFWIRLLLVTCGVSALSM 173
DB 115 ELAVPVVHDGALLAFVCGVVTLLQSIYSKSCPDWNSLTTCVVRMAISAVSCAAVPM 174
QY 174 LTCSSVLHSGNFGTDLQKLNHPNEDKGYLVHMTTAAEWSMSFSFFGFFLTIRDPQKI 233
DB 175 IACASLISI-----TKLEWNPKEKDYIYVVSIAECWTVAPGFIFVFLTFIDQFSV 226
QY 234 SLRVEANLH 242
DB 227 TLIRISTEIN 235
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AC QXJLO;
DT 23-NOV-2004, integrated into UniProtKB/TrEMBL.
DT 23-NOV-2004, sequence version 1.
DT 07-FEB-2006, entry version 10.
DE Zgc:101811.
GN ORFNames=zgc:101811;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
NCBI_TaxID=7955;
RN [1]

CC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 CC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Clark S.;
 RL Submitted (DEC-2004) to the EMBL/GenBank/DBSJ databases.
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 CC -----
 CC EMBL; BX890572; CAI11845.1; -, Genomic DNA.
 DR Ensembl; ENSDARG00000045561; Danio rerio.
 DR ZFIN; ZDB-GENE-041010-147; ZGC:101811.
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Query Match 34.2%; Score 476.5; DB 2; Length 240;
 Best Local Similarity 39.7%; Pred. No. 1.5e-31;
 Matches 96; Conservative 43; Mismatches 94; Indels 9; Gaps 3

QY 1 MWFFQOGLSFLPSALVITWSAAAFPSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAML 60
 DB 1 MFWFMEGMCFLPTFLVWSSSTFIISYIALYRQVDVVLPIYISDTGATPESCVCFGFMS 60

QY 61 NIAAVLCIATYIVRYKQVHALSPENVI-IKLNAGLVGLISLCGLSIVANFQKTTLFA 119
 DB 61 TITAFAPATVAYEYKFFVERVHRTGAVPTLNKVSFGIFGSCIGMCLVATFOETTVME 120

QY 120 AHVSGAVLTFMGSLYMFVOTILSYQMPKTHGKQVFIWIRLLLVWCGYSALSMLTCSVV 179
 DB 121 VHDIGALLFFTCGVVYAVIQSVIGYRAPFYGSSKFMCHLRTFFTVAILAAIPTIACGFL 180

QY 180 LHSGNFGTDLRQKLHNPEDKGYVLHMTTAAEWSMSPFFGFFLTIYIRDFOKISLRVEA 239
 DB 181 V-----GT---SKLHWSNDKDYTHIVSVACEWITTSFVFVFFLYIQEFOQFTLKLV 232

QY 240 NL 241
 DB 233 NL 234

RESULT 14
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 DT 15-MAR-2005, integrated into UniProtKB/TrEMBL.
 DT 15-MAR-2005, sequence version 1.
 DT 07-FEB-2006, entry version 7.
 DE MGC108229 protein.
 GN Name=MGC108229;
 OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
 OC Xenopodinae; Xenopus; Silurana.
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 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Whole body;
 EC MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.2426038999;
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 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalta D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

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RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Whole body;
RA Klein S., Gerhard D.S.;
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
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DR EMBL; BC090386; AAH90386.1; -; mRNA.
SQ SEQUENCE 239 AA; 26578 MW; 2504EC8C84A34DA8 CRC64;

Query Match 34.0%; Score 473.5; DB 2; Length 239;
Best Local Similarity 39.4%; Pred. No. 2.7e-31;
Matches 95; Conservative 55; Mismatches 82; Indels 9; Gaps 4;

QY 3 WFOQGLSFLPSALVIWTSAAFIYSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAMLNI 62
DB 4 WCLGGAALPILVWSSAGFLFSYIISVLIGHVPPFVPIYISDTGTSPESGVFGFMISL 63

QY 63 AAVLCIATIVYRYKQVHALSPENVI-IKLNKAGLVGLSCLGLSIVANFOKTLFRAH 121
DB 64 SAMLGAATWYTRYKILEKQNHSTDFLPYFNKTSIAIGLLGICGIVATFOEMAVPAVH 123

QY 122 VSGAVLTFGMGLSFLMVFQTLISYQMPKIHGKQVFWIRLLLVWCGVSALSMLTCSVLH 181
DB 124 DAGALITFCGVLYILLQSYISKPCANWTRVTHIRMAISVIAFIAVPM-SVFSVL- 181

QY 182 SGNFGTDLBQKLHNPEDKGYVLHMTTAAEWSMSPFSGFFLTIRDPQKISLRVANL 241
DB 182 SG-----RKRLDWKPSDEGYHYHLTSAICEWTVAFGNMYFLTIRDPQGVSIQISTEI 235

QY 242 H 242
DB 236 H 236

RESULT 15
Q6NR56_XENLA PRELIMINARY; PRT; 287 AA.
AC Q6NR56;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 10.
DE LOC431986 protein (Fragment).
GN Names:LOC431986;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
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RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Liver;
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RA Strausberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Harte S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
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RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Liver;
MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Liver;
RA Klein S., Strausberg R.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; BC070646; AAH70646.1; -; mRNA.
FT NON TER 1
SQ SEQUENCE 287 AA; 31871 MW; 5E9814FA488BE462 CRC64;

Query Match 33.9%; Score 471.5; DB 2; Length 287;
Best Local Similarity 38.0%; Pred. No. 4.8e-31;
Matches 93; Conservative 56; Mismatches 79; Indels 17; Gaps 4;

QY 3 WFOQGLSFLPSALVIWTSAAFIYSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAMLNI 62
DB 52 WCLGGAALPILVWSSAGFLFSYIISVLIGHVPPFVPIYISDTGTSPESGVFGFMISV 111

QY 63 AAVLCIATIVYRYKQVHALSPENVI-IKLNKAGLVGLSCLGLSIVANFOKTL 117
DB 112 SAMLGAATWYTRY-----MILERQNLSDFLPIYFNKISLAIGLFCGIGMIVATFOEMAV 167

QY 118 FAHVSGAVLTFGMGLSFLMVFQTLISYQMPKIHGKQVFWIRLLLVWCGVSALSMLTCS 177
DB 168 PAVHDAGALITFCGVWYLLQSYISKPCANWTRVTHIRMAISVIAFIAVPM-SVFS 227

QY 178 SVLHSGNFGTDLBQKLHNPEDKGYVLHMTTAAEWSMSPFSGFFLTIRDPQKISLRV 237
DB 228 --ILSG-----RKRLDWKPSDEGYHYHLTSAICEWTVAFGNMYFLTIRDPQGVSIQI 279

QY 238 EANLH 242
DB 280 STEIH 284

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